

```

1 MPARRLLLLTLLPGLGIFGSTSTVTLPETLLFVSTLDGSLHAVSKRTG 50
  |||||
1 MPARRLLLLTLLPGLGIFGSTSTVTLPETLLFVSTLDGSLHAVSKRTG 50

51 SIKWTLKEDPVLQVPTHVEEPAFLDPNDGSLYTLGSKNNEGLTKLPFTI 100
  |||||
51 SIKWTLKEDPVLQVPTHVEEPAFLDPNDGSLYTLGSKNNEGLTKLPFTI 100

101 PELVQASPCRSSDGILYMGKKQDIWYVIDLLTGEKQQLSSAFADSLCPS 150
  |||||
101 PELVQASPCRSSDGILYMGKKQDIWYVIDLLTGEKQQLSSAFADSLCPS 150

1151 TSLLYLGRTEYITIMYDTKTRELNRNATYFDYAASLPEDEGDYKMSHFVS 200
  |||||
1151 TSLLYLGRTEYITIMYDTKTRELNRNATYFDYAASLPEDEGDYKMSHFVS 200

201 NGDGLVVTVDSESGDVLWIQNYASPVVAFYVWQREGLRKVMHINVAVETL 250
  |||||
201 NGDGLVVTVDSESGDVLWIQNYASPVVAFYVWQREGLRKVMHINVAVETL 250

```

THE

```

251 RYLTFMSGEVGRITKWKYFPKETEAKSKLTPTLYVGKYSTSLYASPSMV 300
|||||
251 RYLTFMSGEVGRITKWKYFPKETEAKSKLTPTLYVGKYSTSLYASPSMV 300

301 HEGVAVPRGSTPLLEGPQTDGVTIGDKGECVITPSTDVKFDPGLKSKN 350
|||||
301 HEGVAVPRGSTPLLEGPQTDGVTIGDKGECVITPSTDVKFDPGLKSKN 350

351 KNLRLNYWLLIGHHETPLSASTKMLERFPNNLPKHRENVIPADSEKKS F 400
|||||
351 KNLRLNYWLLIGHHETPLSASTKMLERFPNNLPKHRENVIPADSEKKS F 400

401 EE..TLLQMTS 409
|| :|::||
401 EEVINLVDQTS 411

```

FIG. 1 (CONT.)¹

```

5  QLQSVSSAIHLCDKKMELSLNIPVNHGPQEESGSSQLHENSOSPETS 54
   :|||||
313 QLQSVSSAIHLCDKKMELSLNIPVNHGPQEESGSSQLHENSOSPETS 362
      .
55  SLPAPQDNDFLSRKAQDCYFMKLHHCPGNHSDSTISGSQRAAFCDHKTT 104
      |||||
363 SLPAPQDNDFLSRKAQDCYFMKLHHCPGNHSDSTISGSQRAAFCDHKTT 412
      .
105 PCSSAIINPLSTAGNSERLQPGIAQQWIIQSKREDIVNQMTACLNQSLDA 154
      |||||
413 PCSSAIINPLSTAGNSERLQPGIAQQWIIQSKREDIVNQMTACLNQSLDA 462
      .
155 LLSRDLIMKEDYELVSTKPTRTSKVRQLLDTTDIQGEEFAKVIQKLKDN 204
      |||||
463 LLSRDLIMKEDYELVSTKPTRTSKVRQLLDTTDIQGEEFAKVIQKLKDN 512
      .
      205 KQMGLOPYPEILVVSRSPSLNLLQNKSM 232
           |||||
      513 KQMGLOPYPEILVVSRSPSLNLLQNKSM 540

```

FIG. 2

```

1  MADLEAVLADVSYLMAMEKSKATPAARASKILLPEPSIRSVMQYLEDR 50
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1  MADLEAVLADVSYLMAMEKSKATPAARASKILLPEPSIRSVMQYLEDR 50

   . . .
51 GEVTFEKIFSQKLGYLFRDFCLNHLEEARPLVEFYEEIKKYEKLETEEE 100
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
51 GEVTFEKIFSQKLGYLFRDFCLNHLEEARPLVEFYEEIKKYEKLETEEE 100

   . . .
101 RVARREIFDSYIMKELLACSHPFKSATEHVQGHGKQVPPDLFQPYI 150
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
101 RVARREIFDSYIMKELLACSHPFKSATEHVQGHGKQVPPDLFQPYI 150

   .
151 EEICQNLRGDVFQKFIE 167
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
151 EEICQNLRGDVFQKFIE 167

```

FIG. 3

1 MGLVSSKKPDKEKPIKEKDKGQWSPLKVS AQDKDAPPLPPLVFNHLLTPP 50
 |||||
 1 MGLVSSKKPDKEKPIKEKDKGQWSPLKVS AQDKDAPPLPPLVFNHLLTPP 50
 51 PPDEHLDEDKHFVVALYDYAMNDRDLQMLKGEKLQVLKGTGDWWLARSL 100
 |||||
 51 PPDEHLDEDKHFVVALYDYAMNDRDLQMLKGEKLQVLKGTGDWWLARSL 100
 101 VTGREGYVPSNFVARVESLEMERWFFRSQGRKEAERQLLAPINKAGSFLI 150
 |||||
 101 VTGREGYVPSNFVARVESLEMERWFFRSQGRKEAERQLLAPINKAGSFLI 150
 151 RESETNKGAFSLSVKDVTTQGELIKHYKIRCLDEGGYIISPRITFFPSLQA 200
 |||||
 151 RESETNKGAFSLSVKDVTTQGELIKHYKIRCLDEGGYIISPRITFFPSLQA 200
 201 LVQHYS..... 206
 |||||
 201 LVQHYSKKGDLGCQRLTLP CVRPAPQNPWAQDEWEIPRQSLRLVRKLGSG 250
 207 SYKNNMKVAIKTLKEGTMSPEAFLGEANVMKALQHERLVRLY 249
 : |||||
 251 QFGEVWMGYKNNMKVAIKTLKEGTMSPEAFLGEANVMKALQHERLVRLY 300

5/138

FIG. 4

250 AVVTKEPIYIVTEYMARGCLLDFLKTDEGSRLSLPRLIDMSAQIAEGMAY 299
|||||
301 AVVTKEPIYIVTEYMARGCLLDFLKTDEGSRLSLPRLIDMSAQIAEGMAY 350
300 IERMNSIHRDLRAANILVSEALCCKIADEGLARIIDSEYTAQEGAKFPIK 349
|||||
351 IERMNSIHRDLRAANILVSEALCCKIADEGLARIIDSEYTAQEGAKFPIK 400
350 WTAPEAIHFGVFTIKADVWSFGVLLMEVVITYGRVPYPGMSNPEVIRNLER 399
|||||
401 WTAPEAYHFGVFTIKADVWSFGVLLMEVVITYGRVPYPGMSNPEVIRNLER 450
400 GYRMPRPDTCPPPELYRGVIAECWRSRPEERPTFEFLQSVLEDFYTATERQ 449
|||||
451 GYRMPRPDTCPPPELYRGVIAECWRSRPEERPTFEFLQSVLEDFYTATERQ 500
450 YELQP 454
|||||
501 YELQP 505

FIG. 4 (CONT.)

FIG. 5

1 MTRDEALPDSHAQDFYENYEPKEILGRGVSSVRRRCIHKPTSQEYAVKV 50
 |||||
 1 MTRDEALPDSHAQDFYENYEPKEILGRGVSSVRRRCIHKPTSQEYAVKV 50
 . . .
 51 IDVTGGGSFSPPEEVRRELREATLKEVDILRKVSGHPNISIQLKDTYETNTF 100
 |||||
 51 IDVTGGGSFSPPEEVRRELREATLKEVDILRKVSGHPNI.IQLKDTYETNTF 99
 .
 101 FFLVFDLMKRGELED 115
 |||||
 100 FFLVFDLMKRGELED 114

FIG. 6


```

1 VFLGRCSVKEFEKLNRI GEGTYGIVYRARDTQTDEI VALKKVRMDKEKD 50
  |||||
1 VFLGRCSVKEFEKLNRI GEGTYGIVYRARDTQTDEI VALKKVRMDKEKD 50

51 GIPISSLREITLLRLRHPNIVELKEVVVGNHLESIFLVMGYCEQDLASL 100
  |||||
51 GIPISSLREITLLRLRHPNIVELKEVVVGNHLESIFLVMGYCEQDLASL 100

101 LENMPTPFSEAQKCVLQVLRGLQYLHRNFIIHRDLKVSNNLLMTDKGCV 150
  |||||
101 LENMPTPFSEAQKCVLQVLRGLQYLHRNFIIHRDLKVSNNLLMTDKGCV 150

      .
151 KTGGCNLTGQAWSL 163
    ||: :|::|:::
151 KTADFGLARAYGV 163

```

FIG. 7

22 AVGCILAEALLAHRPLLPGTSEIHQIDLIVQLLGTSPSENIWPGFSKLPVLG 71
 |||||
 197 AVGCILAEALLAHRPLLPGTSEIHQIDLIVQLLGTSPSENIWPGFSKLPVLG 246
 72 QYSLRKQPYNNLKHKFPWLSEAGRLRLHFLEFMYDPKKRATAGDCLESSYF 121
 |||||
 247 QYSLRKQPYNNLKHKFPWLSEAGRLRLHFLEFMYDPKKRATAGDCLESSYF 296
 122 KEKPLRLPISGVCEGCREPG 141
 |||||
 297 KEKPLRLPISGVCEGCREPG 316

FIG. 8


```

1 MGEAEKFHYIYSCDLIDINVQLKIGSLEGRQKS YKAVLEDPMLKFSGLY 50
| | | | | | | | | | | | | | | | | | : | | | | | | | | | |
1 MGEAEKFHYIYSCDLIDINVQLKIGSLEGRQKS YNAVLEDPMLKFSGLY 50

51 QETCSDLVYTCQVFAEGKPLALPVRTSYKA FSTRWNWNEWLKL PVKY PDL 100
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
51 QETCSDLVYTCQVFAEGKPSALPVRTSYKA FSTRWNWNEWLKL PVKY PDL 100

101 PRNAQVALTIWDVYGPGKAVPVGGTTVS LFGKYGMFRQGMHDLKVWP NVE 150
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
101 PRNAQVALTIWDVYGPGKAVPVGGTTVS LFGKYGMSRQGMHDLKVWP NVE 150

151 ADGSEPTKTPGRTSS TLSEDQMSRLAKLT KAHRQGHMV KVDWLDR LT FRE 200
| | | | | : | | | | | | | | | | | | | | | | | | | | | |
151 ADGSEPTNTPGRTSS TLSEDQMSRLAKLT KAHRQGHMV KVDWLDR LT FRE 200

201 IEMINESVKRSSNFMYLMGGFRCVKCD DKEYGIVYYEKDGDESSPIL TSF 250
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
201 IEMINESVKRSSNFMYLMGGFRCVKCD DKEYGIVYYEKDGDESSPIL TSF 250

251 ELVKVPDPQMSLENLVESKHHLPRSLRSG PSDHDLDLPYSPRDQLKNIV 300
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
251 ELVKVPDPQMSLENLVESKHHLPRSLRSG PSDHDLDLPYSPRDQLKNIV 300

```

FIG. 10

301 SYPPSKPPTYEEQDLVWEFRYYLTNQDKALTKILTSVIWDLPQEAQALA 350
 |||||
 301 SYPPSKPPTYEEQDLVWEFRYYLTNQDKALTKILTSVIWDLPQEAQALA 350

 351 LLGKWNPMDEVDSLELISSHYTNPTVRRYAVARLRQADDEDLLMYLLQLV 400
 |||||
 351 LLGKWNPMDEVDSLELISSHYTNPTVRRYAVARLRQADDEDLLMYLSQLV 400

 401 QALKYENFDDIKNGLEPTKKDSQSSVSENVSNGINSAEIDSSQIITSPL 450
 |||||
 401 QALKYENFDDIKNGLEPTKKDSQSSVSENVSNGINSAEIDSSQIITSPL 450

 451 PSVSSPPASKTKEVPDGENLEQDLCTFLISRACKNSTLANLYWYVIVE 500
 |||||
 451 PSVSSPPASKTKEVPDGENLEQDLCTFLISRACKNSTLANLYWYVIVE 500

 501 CEDQDTQQRDPKTHEMYLNVMRFRSQALLKGDKSVRVMRSLLAAQQTFVD 550
 |||||
 501 CEDQDTQQRDPKTHEMYLNVMRFRSQALLKGDKSVRVMRSLLAAQQTFVD 550

FIG. 10 (CONT.¹)

```

551 RLVHLMKAVQRESGNRRKKKNERLQALLGDNEKMNLSDVELIPLPLEPVK 600
|||||
551 RLVHLMKAVQRESGNRRKKKNERLQALLGDNEKMNLSDVELIPLPLEPVK 600

601 IRGII PETATL FKSALMPAQLFFKTEDGGKYPVIFKHGDDL RQDQLILQI 650
|||||
601 IRGII PETATL FKSALMPAQLFFKTEDGGKYPVIFKHGDDL RQDQLILQI 650

651 ISLMDKLLRKENLDLKLTPYKVLATSTKKGFMQFIQSVPAEVLDTESI 700
|||||
651 ISLMDKLLRKENLDLKLTPYKVLATSTKKGFMQFIQSVPAEVLDTESI 700

701 QNFFRKYAPSENGPNCISAEVMDTYVKSCAGYCVITYILGVGDRHLDNLL 750
|||||
701 QNFFRKYAPSENGPNCISAEVMDTYVKSCAGYCVITYILGVGDRHLDNLV 750

```

751 LTKTG 755

751 LTKTG 755

FIG. 10 (CONT.)²

```

1 MGEAEKFHYIYSCDLINVLKIGSLEKREQSKYKAVLEDPMLKFSGLY 50
|||||
1 MGEAEKFHYIYSCDLINVLKIGSLEKREQSKYKAVLEDPMLKFSGLY 50

51 QETCSDLYVTCQVFAEGKPLALPVRTSYKAFSTRWNNEWLKLVPKYDDL 100
|||||
51 QETCSDLYVTCQVFAEGKPSALPVRTSYKAFSTRWNNEWLKLVPKYDDL 100

101 PRNAQVALTIWDVYGPCKAVPVGGTTVSLFGKYGMFRQGMHDLKVWPVNE 150
|||||
101 PRNAQVALTIWDVYGPCKAVPVGGTTVSLFGKYGMSRQGMHDLKVWPVNE 150

151 ADGSEPTKTPGRTSSTLSEDOMSRLAKLTKAHRQGMVKVDWLDRLTFRE 200
|||||:|||||
151 ADGSEPTNTPGRTSSTLSEDOMSRLAKLTKAHRQGMVKVDWLDRLTFRE 200

201 IEMINESVKRSSNFMVLMGGFRCVKCDDKEYGIVYYEKDGDESSPILTSF 250
|||||
201 IEMINESVKRSSNFMVLMGGFRCVKCDDKEYGIVYYEKDGDESSPILTSF 250

251 ELVKVPDPQMSLENLVESKHHNLPRSLRSGPSDHDCLKPYSPRDQLKNIV 300
|||||
251 ELVKVPDPQMSLENLVESKHHNLPRSLRSGPSDHDCLKPYSPRDQLKNIV 300

```

FIG. 11

```

301 SYPPSKPPTYEEQDLVWEFRYYLTNQDKALTKILTSVIWDLPQEAQALA 350
|||||
301 SYPPSKPPTYEEQDLVWEFRYYLTNQDKALTKILTSVIWDLPQGAQALA 350
|||||
351 LLGKWNPMDEVESLELISSHYTNPTVRRYAVARLRQADDEDLLMYLLQLV 400
|||||
351 LLGKWNPMDEVESLELISSHYTNPTVRRYAVARLRQADDEDLLMYLSQLV 400
|||||
401 QALKYENFDDIKNGLEPTKKDSQSSVSENVSNGINSAEIDSSQIITSPL 450
|||||
401 QALKYENFDDIKNGLEPTKKDSQSSVSGNVSNNGINSAEIDSSQIITSPL 450
|||||
451 PSVSSPPPAKTKVDPDGENLEQDLCTFLISRACKNSTLANLYYWVKII 500
|||||
451 PSVSSPPPAKTKVDPDGENLEQDLCTFLISRACKNSTLANLYYWYV.IV 499

```

501 FC 502

500 EC 501

FIG. 11 (CONT.)¹

FIG. 12

```

1  MVVFENGLLKIKICEAVSLKPTAWSLRHAVGPRPQTFLDPYIALNVDDSR 50
  |||||
1  MVVFENGLLKIKICEAVSLKPTAWSLRHAVGPRPQTFLDPYIALNVDDSR 50

. . .
51 IGQTATKQKTNPAWHDEFVTDVCNCRKIELAVFHDAPIGYDDFVANTCI 100
  |||||
51 IGQTATKQKTNPAWHDEFVTDVCNCRKIELAVFHDAPIGYDDFVANTCI 100

. . .
101 QFEELLQNGSRHFEDWIDLEPEGRVYVIIDLSSGSSGEVKIPNSAFCEER 150
  |||||
101 QFEELLQNGSRHFEDWIDLEPEGRVYVIIDLSSGSSGEAPKDNEERVFRER 150

151 VEMR 154
  :: |
151 MRPR 154

```

FIG. 13

```

1 MILIPRMLLVFLLLPILSSAKAQVNPAICRYPLMSGGQIPDEDITASS 50
|||||
1 MILIPRMLLVFLLLPILSSAKAQVNPAICRYPLMSGGQIPDEDITASS 50

. . . . .
51 QWSESTAACYGRLDSEEGDGAWCEIPVEPDDLKEFLQIDLHTLHFITLV 100
|||||
51 QWSESTAACYGRLDSEEGDGAWCEIPVEPDDLKEFLQIDLHTLHFITLV 100

. . . . .
101 GTQGRHAGGHGIEFAPMYKINYSRDGTRWISWRNRHGKQVLDGNSNPYDI 150
|||||
101 GTQGRHAGGHGIEFAPMYKINYSRDGTRWISWRNRHGKQVLDGNSNPYDI 150

. . . . .
151 FLKDLPEPIVARFVRFIPVTDHSMNVCMRVELYGCVWLDGLVSNAPAGQ 200
|||||
151 FLKDLPEPIVARFVRFIPVTDHSMNVCMRVELYGCVWLDGLVSNAPAGQ 200

. . . . .
201 QFVLPGGSIIYLNDVYDGAVGYSMTGLGQLTDGVSGLDDFTQTHEYHV 250
|||||
201 QFVLPGGSIIYLNDVYDGAVGYSMTGLGQLTDGVSGLDDFTQTHEYHV 250

. . . . .
251 WPGYDYVGWRNESATNGYIEIMFEEDRIRNFTTMKVHCNNMFAKGVKIFK 300
|||||
251 WPGYDYVGWRNESATNGYIEIMFEEDRIRNFTTMKVHCNNMFAKGVKIFK 300

```

FIG. 14

301 EVQCYFRSEASEWEPNAISFPLVLDDVNPSAREFVTVPLHHRMASAIKCQY 350
 |||||
 301 EVQCYFRSEASEWEPNAISFPLVLDDVNPSAREFVTVPLHHRMASAIKCQY 350
 |||||
 351 HFADTWMMFSEITFQSDAAMYNNSALPTSPMAPTTYDPMMLKVDDSNTRI 400
 |||||
 351 HFADTWMMFSEITFQSDAAMYNNSALPTSPMAPTTYDPMMLKVDDSNTRI 400
 |||||
 401 LIGCLVAIIFILLAIIVILWRQWQKMLEKASRRMLDDEMTVSLSPSD 450
 |||||
 401 LIGCLVAIIFILLAIIVILWRQWQKMLEKASRRMLDDEMTVSLSPSD 450
 |||||
 451 SSMFNNRRSSSPSEQGSNSTYDRIFPLRPDYQEPSRLIRKLPEFAPGEEE 500
 |||||
 451 SSMFNNRRSSSPSEQGSNSTYDRIFPLRPDYQEPSRLIRKLPEFAPGEEE 500
 |||||
 501 SG.....EDDVE.QGVKGETSASI 519
 || | |: | | | : | :
 501 SGCSGVVKPVQPSGPEGVPHYAEADIVNLQGVTTGGNTYSV 540

FIG. 14 (CONT.¹)

```

1 MANFQEHLSGSSPHLPFSESKTFNGLQDELTAMGNHSPKLLDQQKEG 50
|||||
1 MANFQEHLSGSSPHLPFSESKTFNGLQDELTAMGNHSPKLLDQQKEG 50

. . .
51 MVRTELIESVHSPVTTTTLTSVSEDSRDQFENSVLQRLREHDESETAVSQG 100
|||||
51 MVRTELIESVHSPVTTTTLTSVSEDSRDQFENSVLQRLREHDESETAVSQG 100

. . .
101 NSNTVDGESTGTEDIKIQFSRSGSGGFGLEGLFGCLRPVWNIIGKAYS 150
|||||
101 NSNTVDGESTGTEDIKIQFSRSGSGGFGLEGLFGCLRPVWNIIGKAYS 150

. . .
151 TDYKFMQQDTWEVPFEEISELQWLGSQAQGAFLGKFRAEEVAIKKVREQ 200
|||:|||||
151 TDYKLQQQDTWEVPFEEISELQWLGSQAQGAFLGKFRAEEVAIKKVREQ 200

. . .
201 NETDIKHLRKLKHPNIIAFKGVCTQAPCYCIIMEYCAHGQLYEVLGRK 250
|||||
201 NETDIKHLRKLKHPNIIAFKGVCTQAPCYCIIMEYCAHGQLYEVLGRK 250

. . .
251 ITPRLLVDWSTGIASGMNYLHLHKIHRDLKSP 283
|||||
251 ITPRLLVDWSTGIASGMNYLHLHKIHRDLKSP 283

```

FIG. 15

```

21 KSGNKS VHLRKASSPNLHRRQWEKNVPNTALTALENASILTSSLTAEDDR 70
   ::|||||
295 EKGNKS VHLRKASSPNLHRRQWEKNVPNTALTALENASILTSSLTAEDDR 344

   . . .
71 GGSVIKYSKN TTRKQWLKETPD TLLN ILKNADLSLAFQTYTYIRPGSEGF 120
   |||||||
345 GGSVIKYSKN TTRKQWLKETPD TLLN ILKNADLSLAFQTYTYIRPGSEGF 394

   . . .
121 LKGPLSEETEASD SV DGGHDSVILDPERLEPGLDEEDTD FEEEDDNP DWV 170
   |||||||
395 LKGPLSEETEASD SV DGGHDSVILDPERLEPGLDEEDTD FEEEDDNP DWV 444

   .
171 SELKKRAGWQGLCDR 185
   |||||||
445 SELKKRAGWQGLCDR 459

```

FIG. 16

```

1  MAPPEETPLIPQQRSCSLLSTEAGALHVLLPARGPGPPQRLSFG 46
    | | | | | | | | | | | | | | | | | | | | | | | | | |
1  MAPPEETPLIPQQRSCSLLSTEAGALHVLLPARGPGPPQRLSFG 46

```

FIG. 17

```

1 MAESAGASSFFPLVLLLAGSGGSGPRGVQALLCACTSCLQANYTCETDG 50
  |||||
1 MAESAGASSFFPLVLLLAGSGGSGPRGVQALLCACTSCLQANYTCETDG 50

51 ACMVSI FNLDGMEHHVRTCIPKVELVPAGKPFYCLSSDLRNTHCCYTDY 100
  |||||
51 ACMVSI FNLDGMEHHVRTCIPKVELVPAGKPFYCLSSDLRNTHCCYTDY 100

101 CNRIDLRVPSGHLKEPEHPSMWGPVELVGIIAGPVFLFLIIIVFLVIN 150
  |||||
101 CNRIDLRVPSGHLKEPEHPSMWGPVELVGIIAGPVFLFLIIIVFLVIN 150

151 YHQRVYHNQRQLDMEDPSCMCLSKDKTQLQDLVYDLSTSGSGSGTKFF 198
  |||||
151 YHQRVYHNQRQLDMEDPSCMCLSKDKTQLQDLVYDLSTSGSGSGGLPLF 198

```

FIG. 18


```

1 MDEQEALNSIMNDLVALQMNRRHRMPGYETMKNKDTGHSNRQSDVRIKFE 50
  |||||
1 MDEQEALNSIMNDLVALQMNRRHRMPGYETMKNKDTGHSNRQSDVRIKFE 50

51 HNGERRIAFSRPVKYEDVEHKVTTVFGQPLDLHYMNNELSILLKNQDDL 100
  |||||
51 HNGERRIAFSRPVKYEDVEHKVTTVFGQPLDLHYMNNELSILLKNQDDL 100

101 DKAIDILDRSSSMKSLRILLLSQDRNHNSSSPHSEVSRQVRIKASQAGD 150
  |||||
101 DKAIDILDRSSSMKSLRILLLSQDRNHNSSSPHSEVSRQVRIKASQAGD 150

151 INTIYQPPEPRSRHLSVSSQNPGRSSPPPGYVPERQQHIARQGSYTSINS 200
  |||||
151 INTIYQPPEPRSRHLSVSSQNPGRSSPPPGYVPERQQHIARQGSYTSINS 200

201 EGEFIPETSEQCMLDPLSSAENSLSGSCQSLDRSADSPSFRKSRMSRAQS 250
  |||||
201 EGEFIPETSEQCMLDPLSSAENSLSGSCQSLDRSADSPSFRKSRMSRAQS 250

```

FIG. 19

```

251 FPDNRQEYSDRETQLYDKGVKGGTYPRRYHVSVHHKDYSDGRRTFPRIRR 300
    |||||
251 FPDNRQEYSDRETQLYDKGVKGGTYPRRYHVSVHHKDYSDGRRTFPRIRR 300
    |||||
301 HQGNLFTLVPSSRSLSTNGENMGLAVQYLDPRGRRLRSADSENALSVMQERN 350
    |||||
301 HQGNLFTLVPSSRSLSTNGENMGLAVQYLDPRGRRLRSADSENALSVMQERN 350
    |||||
351 VPTKCEELSLARRRRLPRWSQTSYGGKQLG 379
    ||| : : ||
351 VPTKSPSAPINWRR.....GKLLG 369

```

FIG. 19 (CONT.¹)

```

1 MDEQEALNSIMNDLVALQMNRRHRMPGYETMKNKDTGHSNRQKKHNSSSS 50
  |||||
1 MDEQEALNSIMNDLVALQMNRRHRMPGYETMKNKDTGHSNRQ..... 42

51 ALLNSPTVTSSCAGASEKKKFLSDVRIKFEHNGERRIIAFSRPVKYEDV 100
  |||||
43 .....SDVRIKFEHNGERRIIAFSRPVKYEDV 69

101 EHKVTVFGQPLDLHYMNNELSILLKNQDDLDKAIDILDRSSSMKSLRIL 150
  |||||
70 EHKVTVFGQPLDLHYMNNELSILLKNQDDLDKAIDILDRSSSMKSLRIL 119

151 LLSQDRNHNSSPHSEVSRQVRIKASQAGDINTIYQPPPEPRSRHLSVSS 200
  |||||
120 LLSQDRNHNSSPHSEVSRQVRIKASQAGDINTIYQPPPEPRSRHLSVSS 169

201 QNPGRSSPPGYVPERQQHIARQGSYTSINSEGEFIPETSEQCMLDPLSS 250
  |||||
170 QNPGRSSPPGYVPERQQHIARQGSYTSINSEGEFIPETSEQCMLDPLSS 219

```

FIG. 20

```

251 AENSLGSCQSLDRSADSPFRKSRMSRAQFDPNQRQEYSDRETQLYDKG 300
    |||||
220 AENSLGSCQSLDRSADSPFRKSRMSRAQFDPNQRQEYSDRETQLYDKG 269
    .
301 VKGGTYPRRYHVSVHHKDYSDGRRTFPRIRRHQGNLFTLVPSSRSLSTNG 350
    |||||
270 VKGGTYPRRYHVSVHHKDYSDGRRTFPRIRRHQGNLFTLVPSSRSLSTNG 319
    .
351 ENMGLAVQYLDPRGRLRSADSENALSVQERNVPTKCEELSLARRRLPRWS 400
    |||||
320 ENMGLAVQYLDPRGRLRSADSENALSVQERNVPTKSPSAPINWRR..... 364
    .
    401 QTSYGGKQLG 410
        |||
    365 .....GKLLG 369

```

FIG. 20 (CONT.¹)

```

1 MAKQYDSVECPFCDEVSKYEKIAKIGQGTGGEVFKARHRKTGQKVALKKV 50
  |||||
1 MAKQYDSVECPFCDEVSKYEKIAKIGQGTGGEVFKARHRKTGQKVALKKV 50

51 LMENEKEGFPITALREIKILQLLKHENVVNLIEICRTKASPNRCKGSIY 100
  |||||
51 LMENEKEGFPITALREIKILQLLKHENVVNLIEICRTKASPNRCKGSIY 100

101 LVDFCFEHDLAGLLSNVLVKFTLSEIKRVMQMLLNGLYY..... 139
  |||||
101 LVDFCFEHDLAGLLSNVLVKFTLSEIKRVMQMLLNGLYYIHRNKILHRDM 150

139 ..... 139

151 KAA NVLI TRDGV LKLAD FGLARAFSLAKNSQPNRYTNRVVTLWYRPPELL 200

139 ..... 139

201 LGERDYGPPI DLWGAGCIMAEMWTRSPIMQGNTEQHQLALISQLCGSITP 250

```

FIG. 21

```

139 ..... 139
251 EVWPNVDNYELYEKLVLKVGQKRKVKDRLKAYVRDPYALDLIDKLLVLDP 300
140 .....NHDFFWSDPMPSDLKGMLSTHLTSMFEYLAPPRKGSQIT 179
    |||||
301 AQRIDSDALNHDFFWSDPMPSDLKGMLSTHLTSMFEYLAPPRKGSQIT 350

    .
180 QQSTNQSRNPATTNQTEFERVF 201
    |||||
351 QQSTNQSRNPATTNQTEFERVF 372

```

FIG. 21 (CONT.¹)

```

1 MATSRYEPVAEIGVGAYGTVYKARDPHSGHFCALKSVRVPNGGGGGGLP 50
  |||||
1 MATSRYEPVAEIGVGAYGTVYKARDPHSGHFVALKSVRVPNGGGGGGLP 50
  |||||

51 ISTVREVALRRLEAFEHPNVVRLMDVCATSRDREIKVTLVFEHVDQDL 100
  |||||
51 ISTVREVALRRLEAFEHPNVVRLMDVCATSRDREIKVTLVFEHVDQDL 100
  |||||

101 RTYLDKAPPPGLPAETIK 118
  |||||
101 RTYLDKAPPPGLPAETIK 118
  
```

FIG. 22

34 PLPLEPRAVYCKDVLIDIEQFSTVKGVNLDHTDDDFYSKFSTGVSIPWQN 83
|: :|||||
464 PFVPPRAVYCKDVLIDIEQFSTVKGVNLDHTDDDFYSKFSTGVSIPWQN 513
84 EMIETECFKELNVFGPNGLPPDLNRNHPPEPPKGLLQRLFKRQHQNNS 133
|
514 EMIETECFKELNVFGPNGLPPDLNRNHPPEPPKGLLQRLFKRQHQNNS 563
134 KSSPSSKTSFNHHINSNHVSSNSTGSS 160
|
564 KSSPSSKTSFNHHINSNHVSSNSTGSS 590

FIG. 24

FIG. 25

```

30  LLSPSGHIRISDLGLAVKIPEGDLIRGRVGTGYMAPEVLNNQRYGLSPD 79
    ||: ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
318 LLDDYGHIRISDLGLAVKIPEGDLIRGRVGTGYMAPEVLNNQRYGLSPD 367

    . . .
80  YWGLGCLYEMIEGQSPFRGRKEKVKREEVDRRVLETEEVYSHKFSEEAK 129
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
368 YWGLGCLYEMIEGQSPFRGRKEKVKREEVDRRVLETEEVYSHKFSEEAK 417

    .
130 SICKMVSSWWPDATLKLVAPSLGLAPV 156
    ||||| : || :| :| :| |
418 SICKMLLT..KDAKQRLGCQEEGAAEV 442

```

FIG. 26

```

1  MAPFLRIAFNSYELGSLQAEDEANQPFCAVKMKEALSTERGKTLVQKKPT 50
  |||||
1  MAPFLRIAFNSYELGSLQAEDEANQPFCAVKMKEALSTERGKTLVQKKPT 50

51  MYPEWKSTFDAHIYEGRVIQIVLMRAAEEPSEVTVGVSVLAERCKKNNG 100
  |||||
51  MYPEWKSTFDAHIYEGRVIQIVLMRAAEEPSEVTVGVSVLAERCKKNNG 100

101  KAEFWLDLQPPQAKVLSVQYFLEDVDCKQSMRSEDEAKFPTMNRRAIKQ 150
  |||||
101  KAEFWLDLQPPQAKVLSVQYFLEDVDCKQSMRSEDEAKFPTMNRRAIKQ 150

151  AKIHYIKNHEFIATFFGQPTFCSVCKDFWGLNKQGYKCRQCNAAIHKKC 200
  |||||
151  AKIHYIKNHEFIATFFGQPTFCSVCKDFWGLNKQGYKCRQCNAAIHKKC 200

201  IDKIIGRCTGTAANSRDTIFQKERFNIDMPHRFKVHNYSPTFCDHCGSL 250
  |||||
201  IDKIIGRCTGTAANSRDTIFQKERFNIDMPHRFKVHNYSPTFCDHCGSL 250

251  LLPAPHDKHQW.....DCG 264
  |
251  L.....WGLVKQGLKCEDCG 265

```

FIG. 27

37/138

```

1 MDETHPGYGKEVDLEFLVSPSLPCLLSFAGSARHLVPPDSNLFSKLWACG 50
  |||||
203 MDETHPGYGKEVD.....LWACG 220

51 VILFTLLAGSPFWHRRQILMLRMIMEGYQFSSPEWDDRSSTVKDLISR 100
  |||||
221 VILFTLLAGSPFWHRRQILMLRMIMEGYQFSSPEWDDRSSTVKDLISR 270

101 LLQVDPEARLTAEQALQHPFFERCEGSQPNLTPRQRFRAVWTVLAAGR 150
  |||||
271 LLQVDPEARLTAEQALQHPFFERCEGSQPNLTPRQRFRAVWTVLAAGR 320

151 VALSTHRVRPLTKNALLRDPYALRSVRHLIDNCAFRLYGHWVKKEQQR 200
  |||||
321 VALSTHRVRPLTKNALLRDPYALRSVRHLIDNCAFRLYGHWVKKEQQR 370

201 AALFQHRPPGPPIMGPEEEGDSAAITAEAVLVLG 236
  |||||
371 AALFQHRPPGPPIMGPEEEGDSAAITAEAVLVLG 406

```

FIG. 28

```

1  MAFCAMRSSKKTEVNLEAPEPGVEVIFYLSDREPLRLGSGEYTAEEELCI 50
  |||
1  MAFCAMRSSKKTEVNLEAPEPGVEVIFYLSDREPLRLGSGEYTAEEELCI 50
  |||
51  RAAQACRISPLCHNLFALYDENTKLWYAPNRTITVDDKMSLRLHYMRMFY 100
  |||
51  RAAQACRISPLCHNLFALYDENTKLWYAPNRTITVDDKMSLRLHYMRMFY 100
  |||
101  FTNWHGTNDNEQSVWRHSPKKQKNGYEKKKIPDATPLLDASSLEYLFAQG 150
  |||
101  FTNWHGTNDNEQSVWRHSPKKQKNGYEKKKIPDATPLLDASSLEYLFAQG 150
  |||
151  QYDLVKCLAPIRDPKTEQDGHDIENECLGMAVLAISHYAMKKMQLPELP 200
  |||
151  QYDLVKCLAPIRDPKTEQDGHDIENECLGMAVLAISHYAMKKMQLPELP 200
  |||
201  KDISYKRYIPETLNKSIRQRNLLTRMRINNVEKDFLKEFNKKTICDSSVS 250
  |||
201  KDISYKRYIPETLNKSIRQRNLLTRMRINNVEKDFLKEFNKKTICDSSVS 250
  |||
251  THDLKVKYLATLETLTCKHYGAEIFETSMILLISSENEMNWFHSNDGGNVLY 300
  |||
251  THDLKVKYLATLETLTCKHYGAEIFETSMILLISSENEMNWFHSNDGGNVLY 300
  |||

```

FIG. 29

39/138

```

301 YEVMVTGNLGIQWRHKPNVVSVEKEKNLKRKKLENKDKKDEEKNKIREE 350
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
301 YEVMVTGNLGIQWRHKPNVVSVEKEKNLKRKKLENKDKKDEEKNKIREE 350

351 WNNFSFFPEITHIVIKESVVSINKQDNKKMELKLSSHEEALSFVSLVDGY 400
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
351 WNNFSFFPEITHIVIKESVVSINKQDNKKMELKLSSHEEALSFVSLVDGY 400

401 FRLTADAHHYLCTDVAPPLIVHNIQNGCHGPICTEYAINKLREQEGSEEGM 450
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
401 FRLTADAHHYLCTDVAPPLIVHNIQNGCHGPICTEYAINKLREQEGSEEGM 450

451 YVLRWSTDFDNIILMTVTCFEKSEQVQGAQKQFKNFQIEVQKGGRYSLHGS 500
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
451 YVLRWSTDFDNIILMTVTCFEKSEQVQGAQKQFKNFQIEVQKGGRYSLHGS 500

501 DRSFPSLGDMLSHLKKQILRTDNI SFMLKRCCQPKPR 537
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
501 DRSFPSLGDMLSHLKKQILRTDNI SFMLKRCCQPKPR 537

```

FIG. 29 (CONT.)

```

1 1 MGCVQCKDEATKLTEERDGSINQSSGYRYGTDPTPQHYPSTIPNY 50
  |||||
1 1 MGCVQCKDEATKLTEERDGSINQSSGYRYGTDPTPQHYPSTIPNY 50

51 1 NNFHAAGGQGLTVFGGVNSSHTGTLRTRGGTGTTLFVALDYEARTEDD 100
  |||||
51 1 NNFHAAGGQGLTVFGGVNSSHTGTLRTRGGTGTTLFVALDYEARTEDD 100

101 1 LSFHKGEKFQILNSSEGDWEARSLLTGTGYIPSNYVAPVDSIQAEWY 150
  |||||
101 1 LSFHKGEKFQILNSSEGDWEARSLLTGTGYIPSNYVAPVDSIQAEWY 150

151 1 FGKLGKDAERQLLSFGNPRGTFLIRESSTKGAYSLIRDWDDMKGDHV 200
  |||||
151 1 FGKLGKDAERQLLSFGNPRGTFLIRESSTKGAYSLIRDWDDMKGDHV 200

201 1 KHYKIRKLDNGGYIITTRAQFETLQQLVQHYSERAAAGLCCRLVVPCHKGM 250
  |||||
201 1 KHYKIRKLDNGGYIITTRAQFETLQQLVQHYSERAAAGLCCRLVVPCHKGM 250

251 1 PRLTDLVKTKDVWEIPRESLQLIKRLNGQFGEVWMG 288
  |||||
251 1 PRLTDLVKTKDVWEIPRESLQLIKRLNGQFGEVWMG 288

```

FIG. 30


```

1  MGCVQCKDKATKLTEERDGSINQSSGYRYGTDPTPQHYPFSGVTSIPNY 50
   |||||
1  MGCVQCKDKATKLTEERDGSINQSSGYRYGTDPTPQHYPFSGVTSIPNY 50

51  NNFHAAGGQGLTVFEGGVNSSHTGTLRTRGGTGVTLFVALYDYEARTEDD 100
   |||||
51  NNFHAAGGQGLTVFEGGVNSSHTGTLRTRGGTGVTLFVALYDYEARTEDD 100

101 LSFHKGEKFQILNSSEGDWWEARSLTTGETGYIPSNYVAPVDSIQAEWY 150
   |||||
101 LSFHKGEKFQILNSSEGDWWEARSLTTGETGYIPSNYVAPVDSIQAEWY 150

151 FGKLGRKDAERQLLSFGNPRGTFLIRESETTKGAYSLSIRDWDDMKGDHV 200
   |||||
151 FGKLGRKDAERQLLSFGNPRGTFLIRESETTKGSYSLSIRDWDDMKGDHV 200

201 KHYKIRKLDNNGGYIITTRAQFETLQQLVQHYSERAAAGLCCRLVVPCHKGM 250
   |||||
201 KHYKIRKLDNNGGYIITTRAQFETLQQLVQHYSERAAAGLCCRLVVPCHKGM 250

```

FIG. 31

251 PRLDLSVKT KD VWEI PRES LQLIKRLGNGQFGEVWMGTWNGNTKVAIKT 300
|||||
251 PRLDLSVKT KD VWEI PRES LQLIKRLGNGQFGEVWMGTWNGNTKVAIKT 300

301 LKPGTMSPE SFLEEAQIMKKLKHDKLVQLYAVVSEEP IYIVTEYMNKG 348
|||||
301 LKPGTMSPE SFLEEAQIMKKLKHDKLVQLYAVVSEEP IYIVTEYMNKG 348

FIG. 31 (CONT.¹)

50 SLELHKRRKALTEPEARYYLRQIVLGCQYLHRNRVIHRDLKLGNLFLNE 99
 |||||
 137 SLELHKRRKALTEPEARYYLRQIVLGCQYLHRNRVIHRDLKLGNLFLNE 186
 . . .
 100 DLEVKIGDFGLATKVEYDGERKKTLCTGTPNYIAPEVLSKKGHSEFVDVWS 149
 |||||
 187 DLEVKIGDFGLATKVEYDGERKKTLCTGTPNYIAPEVLSKKGHSEFVDVWS 236
 . . .
 150 IGCIMYTLVVGKPPFETSCLEKTYLRIKKNEYSIPKHINPVAASLIQKML 199
 |||||
 237 IGCIMYTLVVGKPPFETSCLEKTYLRIKKNEYSIPKHINPVAASLIQKML 286
 . . .
 200 QTDPTARPTINELLNDEFFTSGYIPARLPITCLTIPPRFSIAPSSLDPSN 249
 |||||:|||||
 287 QTDPTARPTINELLGDEFFTSGYIPARLPITCLTIPPRFSIAPSSLDPSN 336
 . . .
 250 RKPLTVLNKGLENPLPERPREKEEPVRETGEVVDCHLSDMLQQQLHSVNA 299
 |||||
 337 RKPLTVLNKGLENPLPERPREKEEPVRETGEVVDCHLSDMLQQQLHSVNA 386
 . . .

FIG. 32

300 SKPSERGLVRQEEAEDPACIPFWVSKWVDYSDKYGLGYQLCDNSVGVLF 349
 |||||
 387 SKPSERGLVRQEEAEDPACIPFWVSKWVDYSDKYGLGYQLCDNSVGVLF 436
 . . .
 350 NDSTRLLLYNDGDSLQYIERDGTESYLTVSSHPSNLSMKKITLLKYFRNYM 399
 |||||
 437 NDSTRLLLYNDGDSLQYIERDGTESYLTVSSHPSNLSMKKITLLKYFRNYM 486
 . . .
 400 SEHLLKAGANITPREGDELARLPYLRTWFRTRSAILHLNNGSVQINFFQ 449
 |||||:|||||
 487 SEHLLKAGNITPRQDELARLPYLRTWFRTRSAILHLNNGSVQINFFQ 536
 . . .
 450 DHTKLILCPLMAAVTYIDEKRDERTYRLSLLEEYGCCKELASRLRYARTM 499
 |||||
 537 DHTKLILCPLMAAVTYIDEKRDERTYRLSLLEEYGCCKELASRLRYARTM 586
 .
 500 VDKLLSSRSASNRLKAS 516
 |||||
 587 VDKLLSSRSASNRLKAS 603

FIG. 32 (CONT.¹)

FIG. 33

```

32 ERGLTVAFSILCNTLQPEFSTYLNFCRSLRFDDKPDYSYLRQLFRNLFHR 81
    |: :: ::||: ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
230 EKKMSTPIEVLCKGYPSEFSTYLNFCRSLRFDDKPDYSYLRQLFRNLFHR 279
    .
    82 QGFSYDYVFDWNMLKFGASSQAQPRD 108
        ||| ||| ||| ||| ||| ||| : |:|
    280 QGFSYDYVFDWNMLKFGAARN...PED 303

```

FIG. 34

```

32 ERGLTVAFSILCNTLQPEFSTYLNFCRSLRFDDKPDYSYLRQLFRNLFHR 81
   |: ::: :||: ||||| ||||| ||||| ||||| ||||| |||||
230 EKKMSTPIEVLCKGYPSEFSTYLNFCRSLRFDDKPDYSYLRQLFRNLFHR 279

   . . . . .
82 QGFSYDYVFDWNMLKFG.....GPL.SCQPPALP 109
   ||||| ||||| ||||| ||||| ||||| ||||| |||||
280 QGFSYDYVFDWNMLKFGAARNPEDVDRERHEREERMGLRGSATRALP 329

   . . . . .
110 CGRPQDELGCSPESRGCGGAARTRTRGEDGAATGVDRDPSPAPWPTHGGH 159
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
330 PGPP.....TGATANRLRSAEPVASTPASRIQPA.....GN 361

   . . . . .
160 CQPAPQCRRRARGFHASLP.HPAGWQYFSQSDLAGR 193
   :| | | | | | | | | | | | | | | | | | | | | | | | | | | |
362 TSPRAISRVDREKVMRLHRGAPANVSSSDLTGR 396

```

FIG. 35

167 MLPEDKEADSLRGNISVKAVKKEVEKKLRCLLADLPLPPELPGGDDLKS 216
 |||||
 1 MLPEDKEADSLRGNISVKAVKKEVEKKLRCLLADLPLPPELPGGDDLKS 50

217 PEEKKTATQLHSKRRPK 233
 |||||:|||||
 51 PEEKKTTQLHSKRRPK 67

FIG. 36

1 MSAKVRLLKLEQLLLDGPWRNESALSVEITLLDVLVCLYTECSHSALRRDK 50
 |||||
 1 MSAKVRLLKLEQLLLDGPWRNESALSVEITLLDVLVCLYTECSHSALRRDK 50

51 YVAEFFLEWAKPFTQLVKEMQLHREDFEIIKVI GRGAFGEVAVVKMKNTER 100
 |||||
 51 YVAEFFLEWAKPFTQLVKEMQLHREDFEIIKVI GRGAFGEVAVVKMKNTER 100

101 IYAMKILNKWEMLKRAETACFREERDVLVNGDCQWITALHYAFQDENHLY 150
 |||||
 101 IYAMKILNKWEMLKRAETACFREERDVLVNGDCQWITALHYAFQDENHLY 150

151 LVMDYYVGGDLLTLLSKFEDKLPEDMARFYIGEMVLAIDSIHQHLYVHRD 200
 |||||
 151 LVMDYYVGGDLLTLLSKFEDKLPEDMARFYIGEMVLAIDSIHQHLYVHRD 200

201 IKPDNVLLDVNGHIRLADFGSCLKMNDGTVQSSVAVGTPDYISPEILQA 250
 |||||
 201 IKPDNVLLDVNGHIRLADFGSCLKMNDGTVQSSVAVGTPDYISPEILQA 250

FIG. 37

FIG. 37 (CONT.¹)

```

1  MSAKVRLLKLEQLLLDGPWRNESALSVELLDVLVCLYTECSHSALRRDK 50
   |||||
1  MSAKVRLLKLEQLLLDGPWRNESALSVELLDVLVCLYTECSHSALRRDK 50

51 YVAEFLEWAKPFTQLVKEMQLHREDFEIIKVGAFGEVAVVKMKNTER 100
   |||||
51 YVAEFLEWAKPFTQLVKEMQLHREDFEIIKVGAFGEVAVVKMKNTER 100

101 IYAMKIILNKWEMLKRAETACFREERDVLVNGDCQWITALHYAFQDENHLY 150
   |||||
101 IYAMKIILNKWEMLKRAETACFREERDVLVNGDCQWITALHYAFQDENHLY 150

151 LVMDYYVVGDDLTLLSKFEDKLPEDMARFYIGEMVLAIIDSIHQHLYVHRD 200
   |||||
151 LVMDYYVVGDDLTLLSKFEDKLPEDMARFYIGEMVLAIIDSIHQHLYVHRD 200

201 IKPDNVLLDVNGHIRLADFGSCLKMNDGTV 231
   |||||
201 IKPDNVLLDVNGHIRLADFGSCLKMNDGTV 231

```

FIG. 38

1 MELRVGNRYRLGRKIGSGSGFDIYL..... 25
 |||||
 1 MELRVGNRYRLGRKIGSGSGFDIYLGTDIAAGEEVAIKLECVKTKHPQLH 50

 26VGIP TIRWCGAEGDYNVMVMELLGPSLEDLNFCSRKF 63
 |||||
 51 IESKIYKMMQGGVGIP TIRWCGAEGDYNVMVMELLGPSLEDLNFCSRKF 100

 64 SLKTVLLADQMISRIEYIHSKNFIHRDVKPDNFLMGLGKKGNLVYIIDF 113
 |||||
 101 SLKTVLLADQMISRIEYIHSKNFIHRDVKPDNFLMGLGKKGNLVYIIDF 150

 114 GLAKKYRDARTHQHIPYRENKNLTGTARYASINTHLGIEQSRDDLES LG 163
 |||||
 151 GLAKKYRDARTHQHIPYRENKNLTGTARYASINTHLGIEQSRDDLES LG 200

 164 YVLMYFNLGSLPWQGLKAATKRQKYERISEKKMSTPIEVLCKGYPSEFAT 213
 |||||
 201 YVLMYFNLGSLPWQGLKAATKRQKYERISEKKMSTPIEVLCKGYPSEFAT 250

FIG. 39

```

214 YLFCRSLRFDKPDYSYLRQLFRNLFHRQGFSDYVFDWNMLKFGASRA 263
    |||||
251 YLFCRSLRFDKPDYSYLRQLFRNLFHRQGFSDYVFDWNMLKFGASRA 300
    .
264 ADDAERDAGDREERLRHSRNPATRGLPSTASGRLRGRKQVAPPTPLTPTS 313
    |||||: |||||: |||||: |||||: |||||: |||||: |||||: |||||:
301 ADDAERERRDREERLRHSRNPATRGLPSTDSGRLRGTQEVAPPTPLTPTS 350
    .
314 HTANTSPRPVSGMERERKVSMLHRGAPVNISSSDLTGRQDTSRMSTSQI 363
    |||||
351 HTANTSPRPVSGMERERKVSMLHRGAPVNISSSDLTGRQDTSRMSTSQI 400
    .
    364 PGRVASSGLQSVVHR 378
        |||||
    401 PGRVASSGLQSVVHR 415

```

FIG. 39 (CONT.¹)

```

14 TFAAPSFDDKILEVAVFGSMQMAVSRVIRLQHHRIAQCRTVKISILGDE 63
   |||||
817 TFAAPSFDDKILEVAVFGSMQMAVSRVIRLQHHRIAQCRTVKISILGDE 866

64 GVPVQVDGEAWVQPPGYIRIVHKNRAQTLTRDRAFESTLKSWE DKQKCEL 113
   |||||
867 GVPVQVDGEAWVQPPGYIRIVHKNRAQTLTRDRAFESTLKSWE DKQKCEV 916

114 PRPPCSLHPEMLSEEEATQMDQFGQAAGVLIHSIREIAQSHRDM EQELA 163
   |||||
917 PRPPCSLHPEMLSEEEATQMDQFGQAAGVLIHSIREIAQSHRDM EQELA 966

164 HAVNASSKSMDRVYGKPRTTTEGLNC SFVLEMVNNFRALRSETELL SGKM 213
   |||||
967 HAVNASSKSMDRVYGKPRTTTEGLNC SFVLEMVNNFRALRSETE. LLSGKM 1015

214 ALQDPPQKEQLGSALAEMDRQLRRRLADTPWLCQSAEPGDEESV MLDLAK 263
   |||||
1016 ALQDPPQKEQLGSALAEMDRQLRRRLADTPWLCQSAEPGDEESV MLDLAK 1065

```

FIG. 40

264 RSRSGKFRRLVTKFKKEKNKNKNEAHSSLGAPVHLWGTEEVAAWLEHLSL 313
 |||||
 1066 RSRSGKFRRLVTKFKKEKNKNKNEAHSSLGAPVHLWGTEEVAAWLEHLSL 1115
 314 EYKDI FTRHDIRGSELLHLERRDLKDLGVTKVGHMKRILCGIKELSRSA 363
 |||||
 1116 EYKDI FTRHDIRGSELLHLERRDLKDLGVTKVGHMKRILCGIKELSRSA 1165

364 AVEA 367
 ||||
 1166 AVEA 1169

FIG. 40 (CONT.¹)

FIG. 41

57/138

```

1 MIVHDDVESEPAMTPSKEGTLIVRQTQSASSTLQKHKSSSFTPFIDPRL 50
  |||
751 MIVHDDVESEPAMTPSKEGTLIVRQTQSASSTLQKHKSSSFTPFIDPRL 800

51 LQISPSSGTTVTSVVGFCDCMRPEAIRQDPTRKGSVVNVNPTNTRPQSD 100
  |||
801 LQISPSSGTTVTSVVGFCDCMRPEAIRQDPTRKGSVVNVNPTNTRPQSD 850

101 TPEIRKYKKRFNSEILCAALWGVNLLVGTESGLMLLDRSGQGKVYPLINR 150
  |||
851 TPEIRKYKKRFNSEILCAALWGVNLLVGTESGLMLLDRSGQGKVYPLINR 900

151 RRFQQMDVLEGLNVLVLTISGKKDKLRVYVYLSWLRNKILHNDPEVEKKQGW 200
  |||
901 RRFQQMDVLEGLNVLVLTISGKKDKLRVYVYLSWLRNKILHNDPEVEKKQGW 950

201 TTVGDLEGCVHYKVVKYERIKFLVIALKSSVEVYAWAPKPYHKFMAFKSF 250
  |||
951 TTVGDLEGCVHYKVVKYERIKFLVIALKSSVEVYAWAPKPYHKFMAFKSF 1000

```

FIG. 42

```

251  GELVHKPLLVDLTVEEGQRLKVIYGSCAGFHAVDVDSGSVDIYLPTHIQ 300
    |||||
1001 GELVHKPLLVDLTVEEGQRLKVIYGSCAGFHAVDVDSGSVDIYLPTHIQ 1050
    |||||

301  CSIKPHAIILPNTDGMELLVCYEDEGVYVNTYGRITKDVVLQWGEMPTS 350
    |||||
1051 CSIKPHAIILPNTDGMELLVCYEDEGVYVNTYGRITKDVVLQWGEMPTS 1100
    |||||

351  VAYIRSNQTMGWGEKAIEIRSVETGHLDGVFMHKRAQRLKFLCERNDKVF 400
    |||||
1101 VAYIRSNQTMGWGEKAIEIRSVETGHLDGVFMHKRAQRLKFLCERNDKVF 1150
    |||||

    401  FASVRSGGSSQVYFMTLGRTSLLSW 425
    |||||
    1151 FASVRSGGSSQVYFMTLGRTSLLSW 1175

```

FIG. 42 (CONT.¹)

14	GEVDLTALAKELRAVEDVRPPHKVTDYSSSEESGTTDEEDDDVEQEGAD	63
674	GEVDLTALAKELRAVEDVRPPHKVTDYSSSEESGTTDEEDDDVEQEGAD	723
64	ESTSGPEDTRAASSLNLNGETESVKTMI VHDDVESEPAMTPSKEGTLIV	113
724	ESTSGPEDTRAASSLNLNGETESVKTMI VHDDVESEPAMTPSKEGTLIV	773
114	RQTQSASSTLQKHKSSSFTPFIDPRLLQISPSSGTTVTSVVGFS CDGMR	163
774	RQTQSASSTLQKHKSSSFTPFIDPRLLQISPSSGTTVTSVVGFS CDGMR	823
164	PEAIRQDPTRKGSVVNVNPTNTRPQSDTPEIRKYKKRFNSEILCAALWGV	213
824	PEAIRQDPTRKGSVVNVNPTNTRPQSDTPEIRKYKKRFNSEILCAALWGV	873
214	NLLVGTESGIMLLDRSGQGKVYPLINRRRFQQMDVLEGLNVLVTISGKGD	263
874	NLLVGTESGIMLLDRSGQGKVYPLINRRRFQQMDVLEGLNVLVTISGKGD	923
264	KLRVYYLSWLRNKILHNDPEVEKKQGWTTVGDLGCVHYKVVKYERIKFL	313
924	KLRVYYLSWLRNKILHNDPEVEKKQGWTTVGDLGCVHYKVVKYERIKFL	973

FIG. 43

314 VIALKSSVEVYAWAPKPYHKFMFAKSFGEIVHKPPLLVDLTVEEGQRLKVI 363
 974 VIALKSSVEVYAWAPKPYHKFMFAKSFGEIVHKPPLLVDLTVEEGQRLKVI 1023
 364 YGSCAGFHAVDVDSGSVDIYLPTHIQCSIKPHAIILPNTDGMELLVCY 413
 1024 YGSCAGFHAVDVDSGSVDIYLPTHIQCSIKPHAIILPNTDGMELLVCY 1073
 414 EDEGVYVNTYGRITKDVVLQWGEPTSVAYIRSNQTMGWGEKAIEIRSVE 463
 1074 EDEGVYVNTYGRITKDVVLQWGEPTSVAYIRSNQTMGWGEKAIEIRSVE 1123
 464 TGHLDGVFMHKRAQRLKFLCERNDKVFFASVRSGSSQVYFMTLGRTSL 513
 1124 TGHLDGVFMHKRAQRLKFLCERNDKVFFASVRSGSSQVYFMTLGRTSL 1173

514 SW 515
 1174 SW 1175

FIG. 43 (CONT.)¹⁾

FIG. 44

```

314 KVIYSCAGFHAVDVDSGSVYDIYLPTHIQCSIKPHAIILPNTDGMELL 363
|||||
1021 KVIYSCAGFHAVDVDSGSVYDIYLPTHIQCSIKPHAIILPNTDGMELL 1070

364 VCYEDEGVYVNTYGRITKDVVLQWGEPMPTSVAYIRSNQTMGWGEKAIEIR 413
|||||
1071 VCYEDEGVYVNTYGRITKDVVLQWGEPMPTSVAYIRSNQTMGWGEKAIEIR 1120

414 SVETGHLDGVMHKRAQRLKFLCERNDKVFFASVRSQVYFMTLGRT 463
|||||
1121 SVETGHLDGVMHKRAQRLKFLCERNDKVFFASVRSQVYFMTLGRT 1170

464 SLLSW 468
|||||
1171 SLLSW 1175

```

FIG. 44 (CONT.¹)

```

1 MDCQLSILLLLSCSVLDSFGELIPQPSNEVNLLDSKTIQGELGWISYPSH 50
  |||||
1 MDCQLSILLLLSCSVLDSFGELIPQPSNEVNLLDSKTIQGELGWISYPSH 50

51 GWEEISGVDEHYTPIRTYQVCNVMDHSQNNWLRTNWVPRNSAQKIYVELK 100
  |||||
51 GWEEISGVDEHYTPIRTYQVCNVMDHSQNNWLRTNWVPRNSAQKIYVELK 100

101 FTLRDCNSIPLVLGTCKETFNLYMESDDDDHGVKFRHQFTKIDTIAADE 150
  |||||
101 FTLRDCNSIPLVLGTCKETFNLYMESDDDDHGVKFRHQFTKIDTIAADE 150

151 SFTQMDLGDRILKLNTEIREVGPVNKKGFYLAQDVGACVALSVRVYFK 200
  |||||
151 SFTQMDLGDRILKLNTEIREVGPVNKKGFYLAQDVGACVALSVRVYFK 200

201 KCPFTVKNLAMFPDTPVPMDSQSLVEVRGSCVNNSKEEDPPRMYCSTEGEW 250
  |||||
201 KCPFTVKNLAMFPDTPVPMDSQSLVEVRGSCVNNSKEEDPPRMYCSTEGEW 250

```

FIG. 45

```

251 LVPIGKSCNAGYEERGMQACRPGFYKALDGNMKCAKCPHSSTQEDG 300
|||||
251 LVPIGKSCNAGYEERGMQACRPGFYKALDGNMKCAKCPHSSTQEDG 300
|||||
301 SMNCRCENNYFRADKDPSPMACTRPSPSPRNVISNINETSVILDWSWPLD 350
|||||
301 SMNCRCENNYFRADKDPSPMACTRPSPSPRNVISNINETSVILDWSWPLD 350
|||||
351 TGGRKDVTFNII CKKCGWNIKQCEPCSPNVRF LPRQFGLTNTT VTVTDLL 400
|||||
351 TGGRKDVTFNII CKKCGWNIKQCEPCSPNVRF LPRQFGLTNTT VTVTDLL 400
|||||
401 AHTNYTFEIDAVNGVSELSPPRQFAAVSITTNQAAPSPVLT IKKDRTSR 450
|||||
401 AHTNYTFEIDAVNGVSELSPPRQFAAVSITTNQAAPSPVLT IKKDRTSR 450
|||||
451 NSISLSWQEPHPNGIILDYEVKYYEKQEQETS YTI LRARGTNVTISSLK 500
|||||
451 NSISLSWQEPHPNGIILDYEVKYYEKQEQETS YTI LRARGTNVTISSLK 500
|||||

```

FIG. 45 (CONT.¹)

FIG. 45 (CONT.)

```
6 WGWVAVVKLNADKVFAMKIILNKWEMLKRAETACFREERDVLVNGDNKWI 55  
:  
88 FGEVAVVKLNADKVFAMKIILNKWEMLKRAETACFREERDVLVNGDNKWI 137  
  
56 TTLHYAFQDDNNLYLVMDYVVGDDLTLLSKFEDRLPEDMARFYLAEMVI 105  
:  
138 TTLHYAFQDDNNLYLVMDYVVGDDLTLLSKFEDRLPEDMARFYLAEMVI 187  
  
106 AIDSVHQHLHVHRDIKPDNIIILMDMNGHIRLADFGSCLKLMEDGTVOSSVA 155  
:  
188 AIDSVHQHLHVHRDIKPDNIIILMDMNGHIRLADFGSCLKLMEDGTVOSSVA 237  
  
156 VGTPDYISPEILQAMEDGKGRYGPECDDWSLGVCMEMLYGETPFYAESL 205  
:  
238 VGTPDYISPEILQAMEDGKGRYGPECDDWSLGVCMEMLYGETPFYAESL 287  
  
206 VETYCKIMNHKERFQFPAQVTDVSENAKDLIRRLICSRHRLGONGIEDF 255  
:  
288 VETYCKIMNHKERFQFPAQVTDVSENAKDLIRRLICSRHRLGONGIEDF 337
```

FIG. 46

[illegible]FIG. 46 (CONT.¹)

```

1 MEVDPQQLGMFTGELMSVGMDTFIHRIDSTEVIYQPRRKRAKLGKYL 50
  |||||
1 MEVDPQQLGMFTGELMSVGMDTFIHRIDSTEVIYQPRRKRAKLGKYL 50

.
51 MGDLLGEGSYGKVKEVLDSETLCRRRAVKILKKKKLRRIPNGEANVKKEIQ 100
  |||||
51 MGDLLGEGSYGKVKEVLDSETLCRRRAVKILKKKKLRRIPNGEANVKKEIQ 100

.
101 LLRRLRHKNVIQLVDVLYNEEKQKMYMVMEYCVCGMQEMLDSVPEKRFPV 150
  |||||
101 LLRRLRHKNVIQLVDVLYNEEKQKMYMVMEYCVCGMQEMLDSVPEKRFPV 150

      151 CQAHG 155
      |||||
      151 CQAHG 155

```

FIG. 47

```

1 MEVVDPQQLGMFTGELMSVGMDTFIHRIDSTEVIYQPRRKRAKLI GKYL 50
  |||||
1 MEVVDPQQLGMFTGELMSVGMDTFIHRIDSTEVIYQPRRKRAKLI GKYL 50

51 MGDLLGEGSYGKVKEVLDSETLCRRRAVKILKKKKLRRIPNGEANVKKEIQ 100
  |||||
51 MGDLLGEGSYGKVKEVLDSETLCRRRAVKILKKKKLRRIPNGEANVKKEIQ 100

101 LLRRLRHKNVIQLVDVLYNEEKQKMYMVMEYCVCGMQEMLDSVPEKRFPV 150
  |||||
101 LLRRLRHKNVIQLVDVLYNEEKQKMYMVMEYCVCGMQEMLDSVPEKRFPV 150

151 CQAHGYFCQLIDGLEYLHSQGI VHKDIKPGNLLLTGGTLKISDLGVAE 199
  |||||
151 CQAHGYFCQLIDGLEYLHSQGI VHKDIKPGNLLLTGGTLKISDLGVAE 199

```

FIG. 48

27 VKDFLSQLRSSNRRFSIPESGQGGTMDGFERRTIENQHSRNDVMVSEWLN 76
 |||||:|||||
 301 VKDFLSQLKSSNRRFSIPESGQGGTMDGFERRTIENQHSRNDVMVSEWLN 350
 . . .
 77 KLNLEPPSSVPKKCPSLTKRSRAQEEQVPQAWTAGTSSDSMAQPPQTPE 126
 |||||
 351 KLNLEPPSSVPKKCPSLTKRSRAQEEQVPQAWTAGTSSDSMAQPPQTPE 400
 . . .
 127 TSTERNQMPSTSTGTPSPGPRGNQGAERQGMNWSCRTPEPNPVTGRPLV 176
 |||||
 401 TSTERNQMPSTSTGTPSPGPRGNQGAERQGMNWSCRTPEPNPVTGRPLV 450
 . . .
 177 NIYNC SGVQVGDNNYLTMQQTALPTWGLAPSGKGRGLQHPPPVGSQEGP 226
 |||||
 451 NIYNC SGVQVGDNNYLTMQQTALPTWGLAPSGKGRGLQHPPPVGSQEGP 500
 .
 227 KDPEAWSRPQGWYNHSGK 244
 |||||
 501 KDPEAWSRPQGWYNHSGK 518

FIG. 49

```

30 EEQARELYRRLREKPRDQRTEGDSQEMVRLLLQAIQSFEKKVRVIYQLS 79
   |||||
564 EEQARELYRRLREKPRDQRTEGDSQEMVRLLLQAIQSFEKKVRVIYQLS 613
   |||||

80 KTVVCKQKALELLPKVEEVVSLMNEDEKTVVRLQEKRQKELWNLLKIACS 129
   |||||
614 KTVVCKQKALELLPKVEEVVSLMNEDEKTVVRLQEKRQKELWNLLKIACS 663
   |||||

1130 KVRGPVSGSPDSMNASRLSQPGQLMSQPSTASNLSPEPAKKSEELVAEAH 179
     |||||
664 KVRGPVSGSPDSMNASRLSQPGQLMSQPSTASNLSPEPAKKSEELVAEAH 713
     |||||

180 NLCTLLENAIQDTVREQDQSFTALDWSWLQTETEEHSCLEQAS 222
    |||||
714 NLCTLLENAIQDTVREQDQSFTALDWSWLQTETEEHSCLEQAS 756

```

FIG. 50

```

1 1 MRLTLLCCTWREERMGEESLPCVASCGRQRIYDGQYLQALNADWHADCF 50
  |||||
1 1 MRLTLLCCTWREERMGEESLPCVASCGRQRIYDGQYLQALNADWHADCF 50

51 1 RCCDCSASLSHQYYEKDGQLFCKKDYWARYGESCHGCSEQITKGLVMVAG 100
  |||||
51 1 RCCDCSASLSHQYYEKDGQLFCKKDYWARYGESCHGCSEQITKGLVMVAG 100

101 1 ELKYHPECFICLTGTFIGDGDYTLVEHSKLYCGHCYYQTVVTPVIEQI 150
  |||||
101 1 ELKYHPECFICLTGTFIGDGDYTLVEHSKLYCGHCYYQTVVTPVIEQI 150

151 1 LPDSPGSHLPHTVTLVSI PASSHGKRGLSVSI DPHPGPGCGTEHSHTVR 200
  |||||
151 1 LPDSPGSHLPHTVTLVSI PASSHGKRGLSVSI DPHPGPGCGTEHSHTVR 200

201 1 VQGVDPGCMSPDVKNLSIHVGDRILEINGTPIRNVPLDEIDLLIQETSRL 250
  |||||
201 1 VQGVDPGCMSPDVKNLSIHVGDRILEINGTPIRNVPLDEIDLLIQETSRL 250

```

FIG. 51

[illegible]

351 GQAIKV 356

351 GQAIKV 356

FIG. 51 (CONT.¹)

74/138

```

1 MRLTLCCCTWREERMGEESLPCASCGRIDGQYLQALNADWHADCF 50
| | | | | | | | | | | | | | | | | | | | | | | | | |
1 MRLTLCCCTWREERMGEESLPCASCGRIDGQYLQALNADWHADCF 50

51 RCCDCSASLSHQYEEKDGQLFCKKDYWARYGESCHGCSEQITKGLVMVAG 100
| | | | | | | | | | | | | | | | | | | | | | | | | |
51 RCCDCSASLSHQYEEKDGQLFCKKDYWARYGESCHGCSEQITKGLVMVAG 100

101 ELKYHPECFICLTGTFIGDGTYYTLVEHSKLYCGHCYYQTVVTPVIEQI 150
| | | | | | | | | | | | | | | | | | | | | | | | | |
101 ELKYHPECFICLTGTFIGDGTYYTLVEHSKLYCGHCYYQTVVTPVIEQI 150

151 LPDSPGSHLPHTVTLVSI PASSHGKRGLSVSI DPHGPPGCGTEHSHTVR 200
| | | | | | | | | | | | | | | | | | | | | | | | | |
151 LPDSPGSHLPHTVTLVSI PASSHGKRGLSVSI DPHGPPGCGTEHSHTVR 200

201 VQGVDPGCMSPDVKN SIHVGDRI LEINGTPIRNVPLDEIDLLIQETSRL 250
| | | | | | | | | | | | | | | | | | | | | | | | | |
201 VQGVDPGCMSPDVKN SIHVGDRI LEINGTPIRNVPLDEIDLLIQETSRL 250

```

FIG. 51

```

251 QLTLEHDPHDTLGHGLGPETSPSSPAYTPSGEAGSSARQKPVLRSCSID 300
|||||
251 QLTLEHDPHDTLGHGLGPETSPSSPAYTPSGEAGSSARQKPVLRSCSID 300
|||||

301 RSPGAGSLGSPASQRKDLGRSESLRVVCRPHRIFRPSDLIHGEVLGKGC 350
|||||
301 RSPGAGSLGSPASQRKDLGRSESLRVVCRPHRIFRPSDLIHGEVLGKGC 350
|||||

351 GQAIKV 356
|||||
351 GQAIKV 356

```

FIG. 51 (CONT.¹)

76/138

```

1 1 MRLTLLCCTWREERMGEESGSELPVCASCGQRIYDGQYLQALNADWHADCF 50
  |||||
1 1 MRLTLLCCTWREERMGEESGSELPVCASCGQRIYDGQYLQALNADWHADCF 50

51 1 RCCDCSASLSHQYYEKDGQFLFCKKDYWARYGESCHGCSEQITKGLVMVAG 100
  |||||
51 1 RCCDCSASLSHQYYEKDGQFLFCKKDYWARYGESCHGCSEQITKGLVMVAG 100

101 1 ELKYHPECFICLTTCGTFIGDGDYTLVEHSKLYCGHCYQTVVTPVIEQI 150
  |||||
101 1 ELKYHPECFICLTTCGTFIGDGDYTLVEHSKLYCGHCYQTVVTPVIEQI 150

151 1 LPDSPGSHLPHTVTLVSI PASSHGKRGLSVSI DPHGPPGCGTEHSHTVR 200
  |||||
151 1 LPDSPGSHLPHTVTLVSI PASSHGKRGLSVSI DPHGPPGCGTEHSHTVR 200

201 1 VQGVDPGCMSPDVKN SIVHGDRILEINGTPIRNVPLDEIDLLIQETSRL 250
  |||||
201 1 VQGVDPGCMSPDVKN SIVHGDRILEINGTPIRNVPLDEIDLLIQETSRL 250

```

FIG. 52

301 LSPSA 305

301 RSPGA 305

FIG. 52 (CONT.¹)

```

1 MASDAVQSEPRWSLLEQLGLAGADLAAPGVQQQLELERERLRREIRKEL 50
  |||||
1 MASDAVQSEPRWSLLEQLGLAGADLAAPGVQQQLELERERLRREIRKEL 50

51 KLKEGAENLRRATTDLGRSLGPVELLLRGSSRRLLDHLHQQLQELHAHVVL 100
  |||||
51 KLKEGAENLRRATTDLGRSLGPVELLLRGSSRRLLDHLHQQLQELHAHVVL 100

101 PDPAATHDGPQSPGAGGPTCSATNLSRVAGLEKQLAIELKVKQGAENMIQ 150
  |||||
101 PDPAATHDGPQSPGAGGPTCSATNLSRVAGLEKQLAIELKVKQGAENMIQ 150

151 TYSNGSTKDRKLLLLTAQQMLQDSKTKIDIIRMQLRRALQADQLENQAAPD 200
  |||||
151 TYSNGSTKDRKLLLLTAQQMLQDSKTKIDIIRMQLRRALQAGQLENQAAPD 200

201 DTQGSPDLGAVELRIEELRRHHFRVEHAEGAKNVLLSAAKAPDRKAV 250
  |||||
201 DTQGSPDLGAVELRIEELRRHHFRVEHAEGAKNVLLSAAKAPDRKAV 250

```

FIG. 53

```

251 SEAQKLTESNQKLGLLREALERRLGE L P A D H P K G R L L R E E L A A S S A A F 300
    |||||
251 SEAQKLTESNQKLGLLREALERRLGE L P A D H P K G R L L R E E L A A S S A A F 300

301 STRLAGPFPA THYSTLCKPAPLTGTLEVRVVGCRDLPETIPWNPTPSMGG 350
    |||||
301 STRLAGPFPA THYSTLCKPAPLTGTLEVRVVGCRDLPETIPWNPTPSMGG 350

351 PGTPDSRPPFLSRPARGLYSRGSLGRSSLKAEAE NTSEVSTVLKLDNT 400
    |||||
351 PGTPDSRPPFLSRPARGLYSRGSLGRSSLKAEAE NTSEVSTVLKLDNT 400

401 VVGQTSWKPCGPNAWDQSFTLELERARELELAVFWRDQ RGLCALKFLKLE 450
    |||||
401 VVGQTSWKPCGPNAWDQSFTLELERARELELAVFWRDQ RGLCALKFLKLE 450

451 DFLDNERHEVQLDMEPQGCLVAEVTFRNPVIERIPRLRRQKKIFSKQQGK 500
    |||||
451 DFLDNERHEVQLDMEPQGCLVAEVTFRNPVIERIPRLRRQKKIFSKQQGK 500

```

FIG. 53 (CONT.¹)

[illegible]

FIG. 53 (CONT.)


```

723 ..... 723
751 EGVVKIADFGLCKEGMGYGDRSTFCGTPEFLAPEVLTDTSYTRAVDWWG 800
723 ..... 723
801 LGVLLYMLVGESPFPGDDEEVFDSIVNDEVRYPRFLSAEAGIMRRLL 850
724 .....RLPPPFVPTLSGRTD 738
      |||||
851 RRNPERRLGSSERDAEDVKKQPFRTLGWEALLARRLPPFPVPTLSGRTD 900
      .
739 VSNFDEEFTGEAPTLSPPRDARPLTAAEQAAFLDFDFVAGGC 780
      |||||
901 VSNFDEEFTGEAPTLSPPRDARPLTAAEQAAFLDFDFVAGGC 942

```

FIG. 53 (CONT.³)

82/138

```

1 MASDAVQSEPRWSLLEQLGLAGADLAAPGVQQQLELERERLRREIRKEL 50
  |||||
1 MASDAVQSEPRWSLLEQLGLAGADLAAPGVQQQLELERERLRREIRKEL 50

. . .
51 KLKEGAENLRRATTDLGRSLGPVELLLRGSSRRLLDHLHQQLQELHAHVVL 100
  |||||
51 KLKEGAENLRRATTDLGRSLGPVELLLRGSSRRLLDHLHQQLQELHAHVVL 100

. . .
101 PDPAATHDGPQSPGAGGPTCSATNLSRVAGLEKQLAIELKVKQGAENMIQ 150
  |||||
101 PDPAATHDGPQSPGAGGPTCSATNLSRVAGLEKQLAIELKVKQGAENMIQ 150

. . .
151 TYSNGSTKDRKLLLTAAQMLQDSKTKIDIIRMQLRRALQADQLENQAAPD 200
  |||||
151 TYSNGSTKDRKLLLTAAQMLQDSKTKIDIIRMQLRRALQADQLENQAAPD 200

. . .
201 DTQGSPDLGAVELRIEELRHHFRVEHAEGAENLRLLSAAKAPDRKAV 250
  |||||
201 DTQGSPDLGAVELRIEELRHHFRVEHAEGAENLRLLSAAKAPDRKAV 250

```

FIG. 54

```

. . . . .
251 SEAQEKLTESNQKLGLLREALERRLGELPADHPKGRLLREELAAASSAAF 300
|||||
251 SEAQEKLTESNQKLGLLREALERRLGELPADHPKGRLLREELAAASSAAF 300

. . . . .
301 STRLAGPFPATHYSTLCKPAPLTGTLEVRVVGCRDLPETIPWNPTPSMGG 350
|||||
301 STRLAGPFPATHYSTLCKPAPLTGTLEVRVVGCRDLPETIPWNPTPSMGG 350

. . . . .
351 PGTPDSRPPFLSRPARGLYSRGSLGRSSLKAEAEANTSEVSTVLKLDNT 400
|||||
351 PGTPDSRPPFLSRPARGLYSRGSLGRSSLKAEAEANTSEVSTVLKLDNT 400

```

FIG. 54 (CONT.¹)

FIG. 55

90 LSGASPFLGETKQETLTNISAVNYDFDEEYFSNTSELA~~KDFIR~~LLVKDP 139
 |||||
 211 LSGASPFLGETKQETLTNISAVNYDFDEEYFSNTSELA~~KDFIR~~LLVKDP 260
 |||||
 140 KRRMTIAQSL~~EH~~SWIKAIRRRNV~~R~~GEDSGRKPER~~RR~~LKTT~~RL~~KEYTIKSH 189
 |||||
 261 KRRMTIAQSL~~EH~~SWIKAIRRRNV~~R~~GEDSGRKPER~~RR~~LKTT~~RL~~KEYTIKSH 310
 |||||
 190 SSLPPNNSYADFERFSKVL~~EE~~AAAAEEGLRELQ~~RS~~RR~~L~~CHEDVEALAAIY 239
 |||||
 311 SSLPPNNSYADFERFSKVL~~EE~~AAAAEEGLRELQ~~RS~~RR~~L~~CHEDVEALAAIY 360
 |||||
 240 EEKEAWYREESDSL~~GQ~~DLRRLRQ~~ELL~~KT~~EAL~~KRQAQ~~EE~~AKGALLGTSGLK 289
 |||||
 361 EEKEAWYREESDSL~~GQ~~DLRRLRQ~~ELL~~KT~~EAL~~KRQAQ~~EE~~AKGALLGTSGLK 410
 |||||
 290 RRF~~S~~RL~~N~~RYEALAKQVASEMR~~F~~VQDLVRALEQ~~E~~KLQ~~G~~VECGLR 333
 |||||
 411 RRF~~S~~RL~~N~~RYEALAKQVASEMR~~F~~VQDLVRALEQ~~E~~KLQ~~G~~VECGLR 454
 |||||

FIG. 56

61 GETALHKAACQRNRAVCQLLLVDAGASLRKTD SKGKTPQERAQQAGDPDLA 110
 |||||
 995 GETALHKAACQRNRAVCQLLLVDAGASLRKTD SKGKTPQERAQQAGDPDLA 1044
 .
 111 AYLESRQNYKVIGHEDLETAV 131
 |||||
 1045 AYLESRQNYKVIGHEDLETAV 1065

FIG. 57

```

1 MRGAARLGRPGRSCLPALRAPRPPLLLLLALLPLLPAPGAAAAPAPR 50
  |||||
1 MRGAARLGRPGRSCLPALRAAAP..ALLARCAVAAAAGLRAAARPR 48
  |||||
51 PPELQASAGPSVSLYLSEDEVRRRLIGLDAELYVVRNDLISHYALSFSLL 100
  |||||
49 PPELQASAGPSVSLYLSEDEVRRRLIGLDAELYVVRNDLISHYALSFNLL 98
  |||||
101 VPSETNFLHFTWHAKSKVEYKLGFGQVDNVLAMDMPQVNISVQGEVPRTLS 150
  |||||
99 VPSETNFLHFTWHAKSKVEYKLGFGQVDNVLAMDMPQVNISVQGEVPRTLS 148
  |||||
151 VFRVELSCTGKVDSEVMILMQNLNTVNSSKNFTVLNFKRRKMCYKKLEEV 200
  |||||
149 VFRVELSCTGKVDSEVMILMQNLNTVNSSKNFTVLNFKRRKMCYKKLEEV 198
  |||||
201 KTSALDKNTSRTIYDPVHAAPTSTRVFYISVGVCCAVIFLVAIILAVLH 250
  |||||
199 KTSALDKNTSRTIYDPVHAAPTSTRVFYISVGVCCAVIFLVAIILAVLH 248
  |||||
251 LHSMKRIELDD 261
  ||:|||||
249 LHNMKRIELDD 259

```

56

1 MPQVNISVQGEVPRTL SVFRVELSCTGKVDSEVMILMQNLNTVNSSKNFT 50
 |||||
 132 MPQVNISVQGEVPRTL SVFRVELSCTGKVDSEVMILMQNLNTVNSSKNFT 181
 |||||
 51 VLNFKRRKMCYKKLEEVKTSALDKNTSRTIYDPVHAAPTSTRVFYISVG 100
 |||||
 182 VLNFKRRKMCYKKLEEVKTSALDKNTSRTIYDPVHAAPTSTRVFYISVG 231
 |||||
 101 VCCAVIFLVAIILAVLHLHSMKRIELDDSIASSSSQGLSQPSTQTQYL 150
 |||||:|||||
 232 VCCAVIFLVAIILAVLHLHSMKRIELDDSIASSSSQGLSQPSTQTQYL 281
 |||||
 151 RADTPNNA TPITSSYYPTLRIEKNDLRSVTLLEAKGKVKDIAISRERITL 200
 |||||
 282 RADTPNNA TPITS..YPTLRIEKNDLRSVTLLEAKGKVKDIAISRERITL 329
 |||||
 201 KDV LQEGTFGRIFHGILIDEKDPNKEKQAFVKTVKDQASEIQVTMMLTES 250
 |||||
 330 KDV LQEGTFGRIFHGILIDEKDPNKEKQAFVKTVKDQASEIQVTMMLTES 379
 |||||

FIG. 59

251 CKLRGLHHRNLLPITHVCIEEGEKEKPMVILPYMWNWGNLKLFLRQCKLVEAN 300
 |||||
 380 CKLRGLHHRNLLPITHVCIEEGEKEKPMVILPYMWNWGNLKLFLRQCKLVEAN 429
 301 NPQAISQQDLVHMAIQIACGMSYLARREVIHKDLAARNVCV 340
 |||||
 430 NPQAISQQDLVHMAIQIACGMSYLARREVIHKDLAARNVCV 469

FIG. 59 (CONT.¹)

1 MEAIRTDNQNFASQLREAEARNRDLEAHVRQLQERMELLQAEGATAVTGV 50
 |||||
 484 MEAIRTDNQNFASQLREAEARNRDLEAHVRQLQERMELLQAEGATAVTGV 533
 .
 51 PSPRATDPPSHL.....DGPPAVAVGCQCLVGP.GPMHRRHL 86
 |||||
 534 PSPRATDPPSHMAPRPWLWASARWWGQAPCTAATCCSLPGSLGLAYRR.. 581
 .
 87 LLPARVP...RPGLSEALSLLLFAVVLSRAAALGCIGLVAHAGQLTAVWR 133
 || | ||:| ||| |:: |
 582RFPCSCSP.....LFCLVPPPPWAAALGWWPTPANSPQ..... 612
 .
 134 RPGAARAP 141
 |||: |
 613 .SGAAQEP 619

90/138

FIG. 60

FIG. 61

6 HEDFEFISGTRMRKLAREGQKPPEGFMAPKAWTVLTEYYKSLEKA 50
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
580 HEDFEFILGTRMRKLAREGQKPPEGFMAPKAWTVLTEYYKSLEKA 624

FIG. 62

```

1 MARTTSQLYDAVPIQSSVVLCSPPSPMVRTQTESSTPPGIPGGSRQGP 50
  |||||
1 MARTTSQLYDAVPIQSSVVLCSPPSPMVRTQTESSTPPGIPGGSRQGP 50

51 MDGTAAEPRPGAGSLQHAQPPQPRKKRPEDFKFGKILGEGSFSTVVLAR 100
  |||||
51 MDGTAAEPRPGAGSLQHAQPPQPRKKRPEDFKFGKILGEGSFSTVVLAR 100

101 ELATSREYAIKILEKRHI IKENKVPYVTRERDVMSRLDHPFFVKLYFTFQ 150
  |||||
101 ELATSREYAIKILEKRHI IKENKVPYVTRERDVMSRLDHPFFVKLYFTFQ 150

151 DDEKLYFGLSYAKNGELLKYIRKIGSFDETCTRFYTAIEIVSALEYLHGKG 200
  |||||
151 DDEKLYFGLSYAKNGELLKYIRKIGSFDETCTRFYTAIEIVSALEYLHGKG 200

201 IIHRDLKPENILLNEDMHIQITDFGTAKVLSPEKQ 236
  |||||
201 IIHRDLKPENILLNEDMHIQITDFGTAKVLSPEKQ 236

```

FIG. 63

```
51 LNNFSVASSVMFR 63
   |||||: ::
51 LNNFSVAKCQLMK 63
```

FIG. 64

```

1 MSDVTIVKEGWVQKRGEYIKNWRPRYFLKTDGSFIGYKEKPQDVDLPYP 50
  |||||
1 MSDVTIVKEGWVQKRGEYIKNWRPRYFLKTDGSFIGYKEKPQDVDLPYP 50

. . .
51 LNNFSVAKCQLMKTERPKPNTFIIIRCLQWTTVIERTFHVDTPEREETE 100
  |||||
51 LNNFSVAKCQLMKTERPKPNTFIIIRCLQWTTVIERTFHVDTPEREETE 100

. . .
101 AIQAVADRLQRQEEERMNCSPSTSQIDNIGEEEMDASTTHHKRKTMNDFDY 150
  |||||
101 AIQAVADRLQRQEEERMNCSPSTSQIDNIGEEEMDASTTHHKRKTMNDFDY 150

. . .
151 LKLLGKGTFGKVILVREKASGKYAMKILKKEVIAK 187
  |||||
151 LKLLGKGTFGKVILVREKASGKYAMKILKKEVIAK 187

```

FIG. 65

[illegible]

FIG. 66


```

1  MELLRITYQPAASTKMCEQALGKCGGNSKKRPPQPPEESQPPQSQAQ 50
   |||||||:|||||
1  MELLRITYQPAASTKMCEQALGKCGGDSKKRPPQPPEESQPPQSQAQ 50
   . . .
51  VPPAAPHHHHSHSGPEISRIIVDPTTGKRYCRGKVLGKGFAKCYEMT 100
   |||||||:|||||
51  VPPAAPHHHHSHSGPEISRIIVDPTTGKRYCRGKVLGKGFAKCYEMT 100
   . . .
101 DLTNNKVYAAKIIPHSRVAKPHQREKVCMTLE 132
   |||||||:|
101 DLTNNKVYAAKIIPHSRVAKPHQREKIDKEIE 132

```

FIG. 67

FIG. 68

```

1 MELLRTITYQPAASTKMCEQALGKCGGNSKKKRPQPPEESQPPQSQAQ 50
  ||||| | | | | |
  |||||
  |||||:|||||
1 MELLRTITYQPAASTKMCEQALGKCGGDSKKKRPQPPEESQPPQSQAQ 50
  . . .
51 VPPAAPHHHHHSHSGPEISRIIVDPTTGKRYCRGKVLGKGFAKCYEMT 100
  |||||
  |||||
  |||||
51 VPPAAPHHHHHSHSGPEISRIIVDPTTGKRYCRGKVLGKGFAKCYEMT 100
  . . .
101 DLTNNKVYAAKIIPHRSRVAKPHQREKIDKEIELHRILHHKHVVQFYHYFE 150
  |||||
  |||||
  |||||
101 DLTNNKVYAAKIIPHRSRVAKPHQREKIDKEIELHRILHHKHVVQFYHYFE 150
  .
151 DKENIYILLEYSRR 165
  |||||
151 DKENIYILLEYSRR 165

```

FIG. 69

```

1 MGHALCVCSRGTVIIDNKRYLFIQKLGE GFSYVDLVEGLHDGHFYALKR 50
  |||||
1 MGHALCVCSRGTVIIDNKRYLFIQKLGE GFSYVDLVEGLHDGHFYALKR 50

51 ILCHEQQDREEAQREADMHRLFNHPNII RL VAYCLRERGAKHEAWLLPF 100
  |||||
51 ILCHEQQDREEAQREADMHRLFNHPNII RL VAYCLRERGAKHEAWLLPF 100

```

101 FK 102

101 FK 102

FIG. 70

```

1  MERAI SPGLLVRA LLLLLLLGLAARTVAAGRARGLPAPTAAEAFGLGAAA 50
  |||||
1  MERAI SPGLLVRA LLLLLLLGLAARTVAAGRARGLPAPTAAEAFGLGAAA 50

. . . . .
51  APTSA TRVPAAGAVAAA ETVEDA EALPAAAGEQEP RGPEDDET ELP R 100
  |||||
51  APTSA TRVPAAGAVAAA ETVEDA EALPAAAGEQEP RGPEDDET ELP R 100

. . . . .
101 GRSLV IISTLDGR IAAALDPENHGKKQWDLDVGGSLVSSSLSKPEVFGNK 150
  |||||
101 GRSLV IISTLDGR IAAALDPENHGKKQWDLDVGGSLVSSSLSKPEVFGNK 150

. . . . .
151 MII PSLDGALFQWDRDRESMETVPFTVESLLES SYKFGDDVVLVGGKSLT 200
  |||||
151 MII PSLDGALFQWDRDRESMETVPFTVESLLES SYKFGDDVVLVGGKSLT 200
  . . . . .

```

FIG. 71

201 TYGLSAYSGKVRYICSGCRQWSDMEQEEDILLQRTQKTAVGPR 250
 |||||
 201 TYGLSAYSGKVRYICSGCRQWSDMEQEEDILLQRTQKTAVGPR 250
 .
 251 SGNEKWNFSVGHFELRYIPDMETRAGFIESTFKPNENTEESKIISDVEEQ 300
 |||||
 251 SGNEKWNFSVGHFELRYIPDMETRAGFIESTFKPNENTEESKIISDVEEQ 300
 .
 301 EAAIMDIVIKVSVADWKVMAFSKKGHLEWEYQFCTPIASAWLLKDGV 350
 |||||
 301 EAAIMDIVIKVSVADWKVMAFSKKGHLEWEYQFCTPIASAWLLKDGV 350
 .
 351 PISLFDDTSYTSNDDVLEDEEDIVEAARGATENSVYLGMYRGQLYLQSSV 400
 |||||
 351 PISLFDDTSYTSNDDVLEDEEDIVEAARGATENSVYLGMYRGQLYLQSSV 400
 .
 401 RISEKFPSPKALESVTNENAIIPPTIKWKPLIHSPSRTPVLVGSDEED 450
 |||||
 401 RISEKFPSPKALESVTNENAIIPPTIKWKPLIHSPSRTPVLVGSDEED 450

FIG. 71 (CONT.¹)

451 KCLSNKFSHEEYSNGALSILQYPYDNGYLYLPYYKKRERNKRSTQITVRFL 500
 |||||
 451 KCLSNKFSHEEYSNGALSILQYPYDNGYLYLPYYKKRERNKRSTQITVRFL 500
 501 DNPYKNIRKKDPVLLHWWKEIVATILFCIIATTFIVRRLFHPPHRQ 550
 |||||
 501 DNPYKNIRKKDPVLLHWWKEIVATILFCIIATTFIVRRLFHPPHRQ 550
 551 RKESETQCQTENKYDSVSGEANDSSWNDIKNSGYISRYLTDFEPIQCLGR 600
 |||||
 551 RKESETQCQTENKYDSVSGEANDSSWNDIKNSGYISRYLTDFEPIQCLGR 600
 601 GGFGVVF EAKNKVDDCN YAIKRIRLPNRELAREKVMREV KALAKLEHPGI 650
 |||||
 601 GGFGVVF EAKNKVDDCN YAIKRIRLPNRELAREKVMREV KALAKLEHPGI 650
 651 VRYFNAWLEAPPEKWQEKMD EIW LKDESTDWPLSSPSPMDAPSVKIRMD 700
 |||||
 651 VRYFNAWLEAPPEKWQEKMD EIW LKDESTDWPLSSPSPMDAPSVKIRMD 700

FIG. 71 (CONT.²)

701 PFSTKEHIEIIAPSPQRSRFSVIGISCDQTSSSESQFSPLEFSGMDHEDI 750
|||||
701 PFSTKEHIEIIAPSPQRSRFSVIGISCDQTSSSESQFSPLEFSGMDHEDI 750
751 SESVDAAYNLQDSCLTDCDVEDGTMDGNDEGHSEFELCPSEASPYVRSRER 800
|||||
751 SESVDAAYNLQDSCLTDCDVEDGTMDGNDEGHSEFELCPSEASPYVRSRER 800
801 TSSSIVFEDSGCDNASSKEPKTNRLHIGHNCANKLT 837
|||||
801 TSSSIVFEDSGCDNASSKEPKTNRLHIGHNCANKLT 837

FIG. 71 (CONT.³)


```

1  MGSRAQKSAGNAELWEPLPEGRPRPAGTSSAVSAWASLKLCLRGSGRRQ  50
   |||||
1  MGSRAQKSAGNAELWEPLPEGRPRPAGTSSAVSAWASLKLCLRGSGRRQ  50

51  RLGGRMQPEEGHRLAAGAAVRGAAATVLLRLRDDLNVTLSHFYVKNE  100
   |||||
51  RLGGRMQPEEGHRLAAGAAVRGAAATVLLRLRDDLNVTLSHFYVKNE  100

101 DLEKIGMRPGQRRLWEAVKRRKALCKRKSWMNKVFSGKRLEAEFPPHHS  150
   |||||
101 DLEKIGMRPGQRRLWEAVKRRKALCKRKSWMNKVFSGKRLEAEFPPHHS  150

151 QSTFRKTSPAPGGPAGEGLQSLTCLIGEKLRLLEKLGDSFGVVRGE  200
   |||||
151 QSTFRKTSPAPGGPAGEGLQSLTCLIGEKLRLLEKLGDSFGVVRGE  200

201 WDAPSGKTVS.....  210
   |||||
201 WDAPSGKTVSAVKCLKPDVLSQPEAMDDFIREVNAMHSLDHRNLIRLYG  250

```

FIG. 72

210 210
 251 VLTTPMKMVTTELAPLGSLDLRLRKHQHFLGLTSLRYAVQVAEGMGCYLE 300
 210 210
 301 SKRFIHRDLAARNLLATRDLVKIGDFGLMRALPQNDHVMQEHKVPF 350
 210 210
 351 AWCAPESLKTRTFSHASDTWMFGVTLWEMFTYQEPWIGLNGSILHKID 400
 210 210
 401 KEGERLPRPEDCPQDIYNVMVQCWAHKPEDRPTFVALRDFLEAQPTDMR 450

FIG. 72 (CONT.¹)

[illegible]

FIG. 72 (CONT. 2)

348 DDFEICSINSTLVGAGVPAGPSQGQNTNYAFVPEQARPPPPLEDNLFPPQ 397
 |||||
 698 DDFEICSINSTLVGAGVPAGPSQGQNTNYAFVPEQARPPPPLEDNLFPPQ 747
 |||||
 398 GGGKPPSSAQTAEIFQALQOECMRQLQAPAGSPAPSPGGDDKPQVPPR 447
 |||||
 748 GGGKPPSSAQTAEIFQALQOECMRQLQAP.GSPAPSPGGDDKPQVPPR 796
 |||||
 448 VPIPPRTRPHVQLSPAPPGEEETSQWPGPASPPRVPPREPLSPQGSRTP 846
 |||||
 797 VPIPPRTRPHVQLSPAPPGEEETSQWPGPASPPRVPPREPLSPQGSRTP 547
 |||||
 498 SPLVPPGSSPLPRLSSSPGKTMPTTQSFASDPKYATPQVIQAPGRAGP 895
 |||||
 847 SPLVPPGSSPLPRLSSSPGKTMPTTQSFASDPKYATPQVIQAPGRAGP 597
 |||||
 548 CILPIVRDGKKVSSSTHYLLPERPSYLYRQFLREAQSPPEPTPLPVPL 945
 |||||
 896 CILPIVRDGKKVSSSTHYLLPERPSYLYRQFLREAQSPPEPTPLPVPL

FIG. 72 (CONT.³)

598 LLPPSTPAPAAPTATVRPMPQAAALDPKANFSTNNSNPGARPPPPRATAR 647
 |||||
 946 LLPPSTPAPAAPTATVRPMPQAAALDPKANFSTNNSNPGARPPPPRATAR 995
 648 LPQRCPCPDGPEAGRPADKIQMAMVHGVTTEECQAAALQCHGWSVQACPV 697
 |||||
 996 LPQRCPCPDGPEAGRPADKIQMAMVHGVTTEECQAAALQCHGWSVQACPV 1045
 698 SEGGAALRAGSAAQRECHKVLEMFWDWNLEQAGCHLLGSWGPAAHKKR 743
 |||||
 1046 SEGGAALRAGSAAQRECHKVLEMFWDWNLEQAGCHLLGSWGPAAHKKR 1091

FIG. 72 (CONT.⁴)

1 MASNPERGEILLTELQGDSRSLPFSENVSAVQKLFSDTMVQQKLDIDK 50
 |||||
 1 MASNPERGEILLTELQGDSRSLPFSENVSAVQKLFSDTMVQQKLDIDK 50
 |||||
 51 RIKREIRKELKIKEGAENLRKVTTDKKSLAYVDNIIKKSNKKLEELHHKL 100
 |||||
 51 RIKREIRKELKIKEGAENLRKVTTDKKSLAYVDNIIKKSNKKLEELHHKL 100
 |||||
 101 QELNAHIVVSDPEDITDCPRTPTDTPNNDPRCSTSNRLKALQKQLDIELK 150
 |||||
 101 QELNAHIVVSDPEDITDCPRTPTDTPNNDPRCSTSNRLKALQKQLDIELK 150
 |||||
 151 VKQGAENMIQMYSGSSKDRKLHGTAQQLQDSKTKIEVIRMQILQAVQT 200
 |||||
 151 VKQGAENMIQMYSGSSKDRKLHGTAQQLQDSKTKIEVIRMQILQAVQT 200
 |||||
 201 NELAFDNAKPVISPLELRMEELRHHFRIEFAVAEGAKNVMKLLGSGKVTD 250
 |||||
 201 NELAFDNAKPVISPLELRMEELRHHFRIEFAVAEGAKNVMKLLGSGKVTD 250
 |||||
 251 RKALSEAQAARFNESSQKLDLLKYSLEQRLNEVPKNHPKSRIIEELSVA 300
 |||||
 251 RKALSEAQAARFNESSQKLDLLKYSLEQRLNEVPKNHPKSRIIEELSVA 300
 |||||

FIG. 73

301 ASPTLSPRQSMISTQNQYSTLSKPAALTGTLEVRIMGCDILENVPGRSK 350
 |||||
 301 ASPTLSPRQSMISTQNQYSTLSKPAALTGTLEVRIMGCDILENVPGRSK 350
 .
 351 ATSVALPGWSPSETRSSFMSTRSKSKSGSSRNLLKTDDLNDVCAVLKLD 400
 |||||
 351 ATSVALPGWSPSETRSSFMSTRSKSKSGSSRNLLKTDDLNDVCAVLKLD 400
 .
 401 NTVVGQTSWKPISNQSWDQKFTLELDRSRELEISVYWRDWRSLCAVKFLR 450
 |||||
 401 NTVVGQTSWKPISNQSWDQKFTLELDRSRELEISVYWRDWRSLCAVKFLR 450
 .
 451 LEDFLDNQRHGMCLYLEPQGTLEAEVTFNPNVIERPKLQKQKIFSKQQ 500
 |||||
 451 LEDFLDNQRHGMCLYLEPQGTLEAEVTFNPNVIERPKLQKQKIFSKQQ 500
 .
 501 GKTELRAPOMNINIAWGRLVRRRAIPTVNHSGTFSPQAPVPTTVPVVDVR 550
 |||||
 501 GKTELRAPOMNINIAWGRLVRRRAIPTVNHSGTFSPQAPVPTTVPVVDVR 550
 .
 551 IPQLAPPA 558
 |||||
 551 IPQLAPPA 558

FIG. 73 (CONT.¹)


```

251 RKALSEAQARFNESSQKDLLKYSLEQRLNEVPKNHPKSRIIIEELSVA 300
|||||
251 RKALSEAQARFNESSQKDLLKYSLEQRLNEVPKNHPKSRIIIEELSVA 300

301 ASPTLSPRQSMISTQNQYSTLSKPAALTGTLEVRIMGCCQDILENVPGRSK 350
|||||
301 ASPTLSPRQSMISTQNQYSTLSKPAALTGTLEVRIMGCCQDILENVPGRSK 350

351 ATSVALPGWSPSETRSSFMSRTSKSKGSSRNLLKTDDLNDVCAVLKLD 400
|||||
351 ATSVALPGWSPSETRSSFMSRTSKSKGSSRNLLKTDDLNDVCAVLKLD 400

401 NTVVGQTSWKPI SNQSWDQKFTLELDRSRELEISVYWRDWRSLCAVKFLR 450
|||||
401 NTVVGQTSWKPI SNQSWDQKFTLELDRSRELEISVYWRDWRSLCAVKFLR 450

```

FIG. 74 (CONT.¹)

```

451 LEDFLDNQRHGMCLYLEPQGTLEAEVTFEFPVIERRKLQKQKIFSKQQ 500
|||||
451 LEDFLDNQRHGMCLYLEPQGTLEAEVTFEFPVIERRKLQKQKIFSKQQ 500
|||||
501 GKTFLRAPQMNIATWGRLVRRRAIPTVNHSGTFSPQAPVPTTVPVVDVR 550
|||||
501 GKTFLRAPQMNIATWGRLVRRRAIPTVNHSGTFSPQAPVPTTVPVVDVR 550
|||||
551 IPQLAPPASDSTVTKLDFDLEPEPPAPPASSLGEIDESSSELRLVDIPG 600
|||||
551 IPQLAPPASDSTVTKLDFDLEPEPPAPPASSLGEIDESSSELRLVDIPG 600

601 QAS 603
|||
601 QDS 603

```

FIG. 74 (CONT.²)

```

1 MVSSQKLEKPIEMGSSEPLPIADGDRRRKKRRGRATDSLPGKFEDMYKL 50
  |||||
1 MVSSQKLEKPIEMGSSEPLPIADGDRRRKKRRGRATDSLPGKFEDMYKL 50

51 TSELLGEGAYAKVQGA VSLQNGKEYAVKII EKQAGHSRSRVFRE VETLYQ 100
  |||||
51 TSELLGEGAYAKVQGA VSLQNGKEYAVKII EKQAGHSRSRVFRE VETLYQ 100

101 CQGNKNILELIEFFEDDTRFYLVFEKLQGGT 131
  |||||
101 CQGNKNILELIEFFEDDTRFYLVFEKLQGGG 131

```

FIG. 75

```

63 MVSSQKLEKPIEMGSSEPLPIADGDRRRKKRRGRATDSLPGKFEDMYKL 112
   |||||
1  MVSSQKLEKPIEMGSSEPLPIADGDRRRKKRRGRATDSLPGKFEDMYKL 50

      113 TSELLGEGAYAKVQGA VSLQNGKEYAVKV 141
      |||||
      51 TSELLGEGAYAKVQGA VSLQNGKEYAVKI 79

```

FIG. 76

```

1  MSGMKLNNSCTPITTPELTTPCGSAEYMAPEVVEVFTDQATFYDKRCDL 50
   :|||||
194 LGSGMKLNNSCTPITTPELTTPCGSAEYMAPEVVEVFTDQATFYDKRCDL 243

   . . .
51  WSLGVVLYIMLSGYPPFVGHCAGDCGWDRCGEVCRVCQNKLFESIQEGKYE 100
   |||||
244 WSLGVVLYIMLSGYPPFVGHCAGDCGWDRCGEVCRVCQNKLFESIQEGKYE 293

   . . .
101 FPDKDWAHISSEAKDLISKLLVRDAKQRLSAAQVLQHPWVQGQAPEKGLP 150
   |||||
294 FPDKDWAHISSEAKDLISKLLVRDAKQRLSAAQVLQHPWVQGQAPEKGLP 343

   . . .
151 TPQVLQRNSSTMDLTLFAAEAIALNRQLSQHEENELAEPEALADGLCSM 200
   |||||
344 TPQVLQRNSSTMDLTLFAAEAIALNRQLSQHEENELAEPEALADGLCSM 393

   . . .
201 KLSPPCKSRLARRRALAQAGGEDRSPPPTAL 231
   |||||
394 KLSPPCKSRLARRRALAQAGGEDRSPPPTAL 424

```

FIG. 77

```

1 MRKGVLDPEIADLFYKDDPEELFIGLHEIGHGSGFAGVYFATNAHTSEVV 50
  |||||
1 MRKGVLDPEIADLFYKDDPEELFIGLHEIGHGSGFAGVYFATNAHTSEVV 50

51 AIKMSYSGKQTHEKWQDILKEVKFLRQLKHPNTIEYKGCYLKEHTAWLV 100
  |||||
51 AIKMSYSGKQTHEKWQDILKEVKFLRQLKHPNTIEYKGCYLKEHTAWLV 100

101 MEYCLGSASDLLLEVHKKPLQEVEIAAITHGALHGLAYLHSHALIHR 146
  |||||
101 MEYCLGSASDLLLEVHKKPLQEVEIAAITHGALHGLAYLHSHALIHR 146

```

FIG. 78

FIG. 79

27 KDLVEEEAEAGVALRSTQSTLQAGLAADAWAAPIAMQIYKKHLDPRPGP 76
|||||
435 KDLVEEEAEAGVALRSTQSTLQAGLAADAWAAPIAMQIYKKHLDPRPGP 484
77 CHLSWAWASWPAAACTAGPKGRPPMTQVYERLEKLQAVVAGVPGHLEA 126
| : : : : : | |||||
485 CPPELGLGLQACCLHRRRAKRRPPMTQVYERLEKLQAVVAGVPGHLEA 534
127 ASCII.PFPQENSYSSTGRAHSGAAPWQPLAAPSGASQAQAEQLQRPNQ 175
||| | |||||
535 ASCII PPSQENSYSSTGRAHSGAAPWQPLAAPSGASQAQAEQLQRPNQ 584
176 PVESDESLGGLSAAALRSWHLTPSCPLDPAPLREAGCPQGD TAGESSWGSG 225
|||||
585 PVESDESLGGLSAAALRSWHLTPSCPLDPAPLREAGCPQGD TAGESSWGSG 634
226 PGSRPTAVEGLALGSSASSSEPPQIIINPARQKMOVQLALYEDGALDSL 275
|||||
635 PGSRPTAVEGLALGSSASSSEPPQIIINPARQKMOVQLALYEDGALDSL 684
276 QLLSSSSLPGLGLEQDRQGPKKVMNFRA 303
||||| : : :
685 QLLSSSSLPGLGLEQDRQGPEESDEFQS 712

FIG. 80

20 Q TQACPPLSWPQRLDILLGTARAIQFLHQDSPSLIHGDIKSSNVLLDERL 69
 |||
 303 Q TQACPPLSWPQRLDILLGTARAIQFLHQDSPSLIHGDIKSSNVLLDERL 352
 . . .
 70 TPKLGDFGLARFSRFAGSSPSQSSMVARTQTVRGTLAYLPPEEYIKTGRLA 119
 |||
 353 TPKLGDFGLARFSRFAGSSPSQSSMVARTQTVRGTLAYLPPEEYIKTGRLA 402
 . . .
 120 VDTDTFSEFGVVVLETLAQRAVKTHGARTKYLKDLVEEEAEEAGVALRST 169
 |||
 403 VDTDTFSEFGVVVLETLAQRAVKTHGARTKYLKDLVEEEAEEAGVALRST 452
 . . .
 170 QSTLQAGLAADAWAAPIAMQIYKKHLDPRPGPCHLSWAWAWASWPAAACT 219
 ||| : : :
 453 QSTLQAGLAADAWAAPIAMQIYKKHLDPRPGPCPPELGLGLQACCCCLH 502
 . . .
 220 AGPKGRPPMTQVYERLEKLQAVVAGVPGHLEAASCI.PFPQENSYVSSTG 268
 | |||
 503 RRAKRRPPMTQVYERLEKLQAVVAGVPGHLEAASCIPPSPQENSYVSSTG 552

FIG. 81

```

269 RAHSGAAPWQPLAAPSGASAAEQLOQGNQPVESDESLGGLSAAALRSW 318
    |||||
553 RAHSGAAPWQPLAAPSGASAAEQLOQGNQPVESDESLGGLSAAALRSW 602
    |||||
319 HLTSCPLDPAPLREAGCPQGDTAGESSWGS GPGSRPTAVEGLALGSSAS 368
    |||||
603 HLTSCPLDPAPLREAGCPQGDTAGESSWGS GPGSRPTAVEGLALGSSAS 652
    |||||
369 SSSEPPQIIINPARQKMVQKLALYEDGALDSLQLLSSSLPGLGLEQDRQ 418
    |||||
653 SSSEPPQIIINPARQKMVQKLALYEDGALDSLQLLSSSLPGLGLEQDRQ 702
    |||||

419 GPKKVMNFRA 428
    ||:: :|::
703 GPEESDEFQS 712

```

FIG. 81 (CONT.¹)

1	MAGPGGEP	AAPGAQHFLYE	VPWVMCRFYK	VMDALEPADWCQFAALIV	50
1	MAGPGGEP	AAPGAQHFLYE	VPWVMCRFYK	VMDALEPADWCQFAALIV	50
51	RDQTELR	CERSGQRTAS	VLWPWINRNAR	VADLVHILTHLQLLRARDIIT	100
51	RDQTELR	CERSGQRTAS	VLWPWINRNAR	VADLVHILTHLQLLRARDIIT	100
101	AWHPPAP	LPSPGTTAPR	SSIPAPAEAE	AWSPRKLPSASTFLSPA	FPGS 150
101	AWHPPAP	LPSPGTTAPR	SSIPAPAEAE	AWSPRKLPSASTFLSPA	FPGS 150
151	QTHSGPE	LGLVSPASL	WPPPPSPAP	SSTKPGP	ESSVLLQGARPSPFCW 200
151	QTHSGPE	LGLVSPASL	WPPPPSPAP	SSTKPGP	ESSVLLQGARPSPFCW 200

FIG. 82

```

201 PLCEISRGTHNFSEELKIGEGGFCVYRAVMRNTVYAVKRLKENADLEWT 250
    |||||
201 PLCEISRGTHNFSEELKIGEGGFCVYRAVMRNTVYAVKRLKENADLEWT 250
    |||||
251 AVKQSFLTEVEQLSRFRHPNIVDFAGYCAQNGFYCLVYGFLPNGSLEDRL 300
    |||||
251 AVKQSFLTEVEQLSRFRHPNIVDFAGYCAQNGFYCLVYGFLPNGSLEDRL 300
    |||||
301 HCQTQACPPPLSWPQRLDILLGTARASQVSCNRVSSCVSKSSPGL 344
    |||||
301 HCQTQACPPPLSWPQRLDILLGTARAIQF.....LHQDSPSL 336

```

FIG. 82 (CONT.¹)

1 MFTEEDVKFYLAELALDHLHLGLIYRDLKPENILLDEEGHIKLTDFG 50
 |||||
 164 MFTEEDVKFYLAELALDHLHLGLIYRDLKPENILLDEEGHIKLTDFG 213
 .
 51 LSKESIDHEKKAYSFCGTVEYMAPEVNVNRRGHTQSADWWSFGVLMFEMLT 100
 |||||
 214 LSKESIDHEKKAYSFCGTVEYMAPEVNVNRRGHTQSADWWSFGVLMFEMLT 263
 .
 101 GTLPFQGKDRKETMTMILKAKLGMPQFLSPEAQSLRLMLFKRNPANRLGA 150
 |||||
 264 GTLPFQGKDRKETMTMILKAKLGMPQFLSPEAQSLRLMLFKRNPANRLGA 313
 .
 151 GPDGVEEIKRHSFFSTIDWNKLYRREIHPPFKPATGRPEDTFYFDPEFTA 200
 |||||
 314 GPDGVEEIKRHSFFSTIDWNKLYRREIHPPFKPATGRPEDTFYFDPEFTA 363
 .
 201 KTPKDSPGIPPSANAHQLFRGFSFVAITSDDESQAMQTVGVHSIVQQLHR 250
 |||||
 364 KTPKDSPGIPPSANAHQLFRGFSFVAITSDDESQAMQTVGVHSIVQQLHR 413
 .
 251 NSIQFTDGYEVKEDIGVGSYVCKRCIHKATNMEFAVKV 289
 |||||:
 414 NSIQFTDGYEVKEDIGVGSYVCKRCIHKATNMEFAVKI 452

FIG. 83

```

1 MPLAQLADPWQKMAVESPSDSAENGQQIMDEPMGEEEEINPQTEEVSIKEI 50
  |||||
1 MPLAQLADPWQKMAVESPSDSAENGQQIMDEPMGEEEEINPQTEEVSIKEI 50

51 AITHHVKEGHEKADPSQFELLKVLGQGSFGKVFVKKISGSDARQLYAMK 100
  |||||
51 AITHHVKEGHEKADPSQFELLKVLGQGSFGKVFVKKISGSDARQLYAMK 100

101 VLKATLKVDRDRVRTKMERDILVEVNHPPFIVKLHYAFQTEGKLYLILDFL 150
  |||||
101 VLKATLKVDRDRVRTKMERDILVEVNHPPFIVKLHYAFQTEGKLYLILDFL 150

151 RGGDLFTRLSKEVMFTEEDVKFYLAELALALDHLHSLGIYYRDLKPE 197
  |||||
151 RGGDLFTRLSKEVMFTEEDVKFYLAELALALDHLHSLGIYYRDLKPE 197

```

FIG. 84

1 MSTEADEGITFSVPPFAPSGFCTIPEGGICRRGGAAAVGEGEEHQLPPPP 50
 |||||
 1 MSTEADEGITFSVPPFAPSGFCTIPEGGICRRGGAAAVGEGEEHQLPPPP 50
 |||||
 51 PGSEWNVESAAAPGIGCPAATSSSSATRGRGSSVGGSSRRTTVAYVINEA 100
 |||||
 51 PGSEWNVESAAAPGIGCPAATSSSSATRGRGSSVGGSSRRTTVAYVINEA 100
 |||||
 101 SQQLVVAESEALQSLREACETVGATLETLHFGKLDFGETTVLDRFYNAD 150
 |||||
 101 SQQLVVAESEALQSLREACETVGATLETLHFGKLDFGETTVLDRFYNAD 150
 |||||
 151 IAVVEMSDAFRQPSLFYHLGVRESFSMANNIILYCDTNSDSLQSLKEIIC 200
 |||||
 151 IAVVEMSDAFRQPSLFYHLGVRESFSMANNIILYCDTNSDSLQSLKEIIC 200
 |||||
 201 QKNTMCTGNYTFVPYMITPHNKVYCCDSSFMMKGLTELMQPNFELLGPIC 250
 |||||
 201 QKNTMCTGNYTFVPYMITPHNKVYCCDSSFMMKGLTELMQPNFELLGPIC 250

FIG. 85

251 LPLVDRFIQLLKVAQASSQYFRESILNDIRKARNLYTGKELAAELARIR 300
 |||||
 251 LPLVDRFIQLLKVAQASSQYFRESILNDIRKARNLYTGKELAAELARIR 300
 |||||
 301 QRVDNIEVLTADIVINLLSYRDIQDYDSIVKLVEKLPFTFDLASHHH 350
 |||||
 301 QRVDNIEVLTADIVINLLSYRDIQDYDSIVKLVEKLPFTFDLASHHH 350
 |||||
 351 VKFHYAFALNRRNLPGDRAKALDIMIPMVQSEGQVADMYCLVGRIYKDM 400
 |||||
 351 VKFHYAFALNRRNLPGDRAKALDIMIPMVQSEGQVADMYCLVGRIYKDM 400
 |||||
 401 FLDSNFTDTESRDHGASWFKKAFESEPTLQSGINYAVLLLAAGHQFESSF 450
 |||||
 401 FLDSNFTDTESRDHGASWFKKAFESEPTLQSGINYAVLLLAAGHQFESSF 450
 |||||
 451 ELRKVG 456
 |||||
 451 ELRKVG 456

FIG. 85 (CONT.¹)

FIG. 86

```
68 IGS.....AAYDAVLDNRNVAIKKLSRPFQNTAKRAYRELVLMLKCVN 110  
    |||      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
70 IGGAQGIVCAAYDAVLDNRNVAIKKLSRPFQNTAKRAYRELVLMLKCVN 119  
  
111 HKNIISLLNVFTPQKTLEEFQDVYLVME LMDANLCQVIQMELDHERMSYL 160  
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
120 HKNIISLLNVFTPQKTLEEFQDVYLVME LMDANLCQVIQMELDHERMSYL 169  
  
161 LYQMLCGIKHLHSAGIIHRDLKPSNIVVKSDCTLKILDFGLARTAGTSFM 210  
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
170 LYQMLCGIKHLHSAGIIHRDLKPSNIVVKSDCTLKILDFGLARTAGTSFM 219  
  
211 MTPYVVTRYRAPEVILGMGYKENVDIWSVGIMGEMVRHKILFPGRDYI 260  
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
220 MTPYVVTRYRAPEVILGMGYKENVDIWSVGIMGEMVRHKILFPGRDYI 269  
  
261 DQWNKVIEQLGTPCPEFMKKLQPTVRNYVENRPKYAGLTFFPKLFPDSLEP 310  
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
270 DQWNKVIEQLGTPCPEFMKKLQPTVRNYVENRPKYAGLTFFPKLFPDSLEP 319
```

FIG. 18

311 ADSEHNKLKASQARDLLSKMLVIDPAKRISVDDALQHPYINVWYDPAEVE 360
 |||||
 320 ADSEHNKLKASQARDLLSKMLVIDPAKRISVDDALQHPYINVWYDPAEVE 369
 361 APPPQIYDKQLDEREHTIEEWKELIYKEVMNSEKTKNGVVKGQSPSAQ 410
 |||||
 370 APPPQIYDKQLDEREHTIEEWKELIYKEVMNSEKTKNGVVKGQSPSAQ 419

411 VQQ 413

|||

420 VQQ 422

131/138

FIG. 87 (CONT.¹)

```

1 MSKSKVDNQFYSVEVG DSTFTVLKRYQNLKPIGSGAQGIVCAAYDAVLDR 50
  |||||
39 MSKSKVDNQFYSVEVG DSTFTVLKRYQNLKPIGSGAQGIVCAAYDAVLDR 88
  .
51 NVAIKKLSRPFQNTAKRAYRELVLKCVNHKNV..... 85
  |||||
89 NVAIKKLSRPFQNTAKRAYRELVLKCVNHKNIIISLLNVFTPPQKTLEE 138
  .
86 ...SFVIFKLLAVGVCKI 100
  :::::|: ::|::
139 FQDVYLVMEI LMDANLCQV 156

```

FIG. 88

133/138

```

1 MAMTGSTPCSSMSNHTKERVTMTKVTLENFYSNLIAQHEEREMRQKKLEK 50
  |||||
1 MAMTGSTPCSSMSNHTKERVTMTKVTLENFYSNLIAQHEEREMRQKKLEK 50

51 VMEEGLKDEEKRLRRSAHARKETEFRLKRTLGLGFESLKVIGRGAF 100
  |||||
51 VMEEGLKDEEKRLRRSAHARKETEFRLKRTLGLGFESLKVIGRGAF 100

101 GEVRLVQKKDTGHVYAMKILRKADMLEKEQVGHIRAERDILVEADSLWVV 150
  |||||
101 GEVRLVQKKDTGHVYAMKILRKADMLEKEQVGHIRAERDILVEADSLWVV 150

151 KMFYSFQDKLNLYLIMEFLPGGDMTLLMKKDTLTHEEETQFYIAETVLAI 200
  |||||
151 KMFYSFQDKLNLYLIMEFLPGGDMTLLMKKDTLTHEEETQFYIAETVLAI 200

201 DSIHQLGFIHRDIKPDNLLDSKGVKLSDFGLCTGLKKAHRTEFYRNLN 250
  |||||
201 DSIHQLGFIHRDIKPDNLLDSKGVKLSDFGLCTGLKKAHRTEFYRNLN 250

```

FIG. 89

251 HSLPSDFTFQNMNSKRKAETWKRNRRLAFSTVGTPDYIAPEVFMQTGYN 300

251 HSLPSDFTFQNMNSKRKAETWKRNRRLAFSTVGTPDYIAPEVFMQTGYN 300

```

301 KLCDWWSLGVIMYEMLIG 318
      |||||
301 KLCDWWSLGVIMYEMLIG 318

```

FIG. 89 (CONT.¹)

11 VSGGSMLDIIKYIVNRGEHKNVLEEAIATILKEVLEGLDYLHRNGQIH 60
 :|||||
 143 LSGGSMLDIIKYIVNRGEHKNVLEEAIATILKEVLEGLDYLHRNGQIH 192
 61 RDLKAGNILLGEDGSVQIADFGVSAFLATGGDVTRNKVVRKTFVGTPCWMA 110
 |||||
 193 RDLKAGNILLGEDGSVQIADFGVSAFLATGGDVTRNKVVRKTFVGTPCWMA 242
 111 PEVMEQVRGYDFKADMWSFGITAIELATGAAPYHKYPPMKVLM LTLQNDP 160
 |||||
 243 PEVMEQVRGYDFKADMWSFGITAIELATGAAPYHKYPPMKVLM LTLQNDP 292
 161 PLETGVEDKEMMKYKGSFRKLLSLCLQKDPSKRPTAAELLKCKFFQKA 210
 |||||
 293 PLETGVEDKEMMKYKGSFRKLLSLCLQKDPSKRPTAAELLKCKFFQKA 342
 211 KNREYLIKLLTRTPDIAQRAKKVRRVPGSSGHLHKTEDGDWESDDMD 260
 |||||
 343 KNREYLIKLLTRTPDIAQRAKKVRRVPGSSGHLHKTEDGDWESDDMD 392

135/138

FIG. 90

261 EKSEEGKAAFSQEKSRVKEENPEIAVSASTIPEQIQSLSVHDSQGPNA 310
 |||||
 393 EKSEEGKAAFSQEKSRVKEENPEIAVSASTIPEQIQSLSVHDSQGPNA 442
 |||||
 311 NEDYREASSCAVNLVLRNRSRKELNDIRFEFTPGRDTADGVSQELFSAG 360
 |||||
 443 NEDYREASSCAVNLVLRNRSRKELNDIRFEFTPGRDTADGVSQELFSAG 492
 |||||
 361 LVDGHDVVIVAANLQKIVDDPKALKTLTFKLASGCDGSEIPDEVKLIGFA 410
 |||||
 493 LVDGHDVVIVAANLQKIVDDPKALKTLTFKLASGCDGSEIPDEVKLIGFA 542
 |||||
 411 QLSVS 415
 |||||
 543 QLSVS 547

FIG. 90 (CONT.¹)


```

11 VSGGSMLDIIKYIVNRGEHKNGVLEEEAIIATILKEVLEGLDYLHRNGQIH 60
:|||||
143 LSGGSMLDIIKYIVNRGEHKNGVLEEEAIIATILKEVLEGLDYLHRNGQIH 192

61 RDLKAGNILLGEDGSVQIADFGVSAFLATGGDVTRNKVRKTFVGTPCWMA 110
|||||
193 RDLKAGNILLGEDGSVQIADFGVSAFLATGGDVTRNKVRKTFVGTPCWMA 242

111 PEVMEQVRGYDFKADMWSFGITAEIATGAAPYHKYPPMKVLMTLQNDP 160
|||||
243 PEVMEQVRGYDFKADMWSFGITAEIATGAAPYHKYPPMKVLMTLQNDP 292

161 PLETGVEDKEMMKYKGSFRKLLSLCLQKDPSKRPTAAELLKCKFFQKA 210
|||||
293 PLETGVEDKEMMKYKGSFRKLLSLCLQKDPSKRPTAAELLKCKFFQKA 342

211 KNREYLIEKLLTRTPDIAQRAKKVRRVPGSSGHLHKTEDGDWESSDDMD 260
|||||
343 KNREYLIEKLLTRTPDIAQRAKKVRRVPGSSGHLHKTEDGDWESSDDMD 392

```

16
G.
H.
H.

261 EKSEEGKAAFSQEKSRVKEENPEIAVSASTIPEIQISLVHDSQGPNA 310
 |||||
 393 EKSEEGKAAFSQEKSRVKEENPEIAVSASTIPEIQISLVHDSQGPNA 442
 |||||
 311 NEDYREASSCAVNLVLRNLSRKELNDRFEFTPGRDTADGVSQELFSAG 360
 |||||
 443 NEDYREASSCAVNLVLRNLSRKELNDRFEFTPGRDTADGVSQELFSAG 492
 |||||
 361 LVDGHDVVIVAANLQKIVDDPKALKTLTFKL 391
 |||||
 493 LVDGHDVVIVAANLQKIVDDPKALKTLTFKL 523

FIG. 91 (CONT.¹)